Listing of Claims

1. (**Currently Amended**) A method for generating at least one error-corrected experiment profile of at least one experiment profile in a plurality of pairs of profiles $\{A_m, C_m\}$, where m = 1, 2, …, M, and M is the number of the pairs of profiles; and wherein, for each m ϵ {1, 2, …, M}, A_m is an experiment profile, and C_m is a reference profile; and wherein $\{A_m\}$ represents experiment profiles in said plurality of pairs of profiles $\{A_m, C_m\}$ and $\{C_m\}$ represents reference profiles in said plurality of pairs of profiles $\{A_m, C_m\}$, said method comprising:

(a) calculating, on a suitably programmed computer, an average reference profile $\bar{C}$ of said plurality of reference profiles $\{C_m\}$ where m = 1, 2, …, M;

(b) determining, on a suitably programmed computer, for at least one profile pair $\{A_m, C_m\}$where m ϵ {1, 2, …, M} of said plurality of pairs of profiles $\{A_m, C_m,\}$ a differential reference profile computed between C_m and $\bar{C}$;

(c) ~~adjusting~~ **via said differential reference profile determined for said profile pair, removing**, on a suitably programmed computer, **systematic cross-experiment error from** an experiment profile A_m of said at least one profile pair $\{A_m, C_m\}$ where m ϵ {1, 2, …, M} ~~based on said differential reference profile determined for said profile pair~~ to generate a first error-corrected experiment profile A'_m for each m ϵ {1, 2, …, M}, wherein said experiment profile A_m comprises a first data set, said reference profile C_m comprises a second data set, said average reference profile $\bar{C}$ comprises data set $\{\bar{C}(k)\}$, and said first error-corrected experiment profile A'_m

comprises data set $\{A'_m(k)\}$; wherein said first data set comprises measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of a plurality of different cellular constituents measured in a sample having been subject to a first condition, said second data set comprises measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents measured in a sample having been subject to a second condition; and wherein k = 1, 2, ..., N; k is an index of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents, N being the total number of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements;

(d) obtaining a data set $\{A''_m(k)\}$, wherein obtaining said data set $\{A''_m(k)\}$ comprises combining said first error-corrected experiment profile A'_m with said experiment profile A_m using a weighing factor $\{w(k)\}$, k = 1, 2, ... , N, wherein $w(k)$ is a weighing factor for the k'th measurement; and

~~(d)~~ **(e)** outputting to a user, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying: said first error-corrected experiment profile A'_m, said data set $\{A'_m(k)\}$, a second error-corrected experiment profile A''_m, or ~~a~~ **said** data set $\{A''_m(k)\}$, wherein said second error-corrected experiment profile A''_m comprises said data set $\{A''_m(k)\}$ ~~**obtained by combining said first error-corrected experiment profile A'_m with said experiment profile A_m using a weighing factor $\{w(k)\}$, k = 1, 2, ... , N, wherein $w(k)$ is a weighing**~~

~~factor for the *k*'th measurement~~.

2. (Previously Presented) The method of claim 1, wherein said steps (b) and (c) are performed for each profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, \ldots, M\}$.

3. (**Currently Amended**) The method of claim 2, wherein each of said experiment profile A_m and said reference profile C_m comprises measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents from the same experimental reaction.

4. (Previously Presented) The method of claim 3, wherein said $\bar{C}(k)$ is calculated according to the equation

$$\bar{C}(k) = \frac{1}{M} \sum_{m=1}^{M} C_m(k)$$

wherein said differential reference profile is determined according to the equation

$$C_{diff}(m,k) = C_m(k) - \bar{C}(k)$$

and wherein said first error-corrected experiment profile A'_m is generated according to the equation

$$A'_m(k) = A_m(k) - C_{diff}(m,k)$$

wherein $\{A_m(k)\}$ is said first data set of experiment profile A_m.

5. **(Currently Amended)** The method of claim 4, further comprising:

(d) calculating, for **one or more remaining profile pairs out of ~~each said~~ said** profile **~~pair~~ pairs** $\{A_m, C_m\}$, **~~said~~ a respective** second error-corrected experiment profile $A"_m$; and

(e) outputting to, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying; said **respective** second error-corrected experiment profile $A"_m$ or said data set $\{A"_m(k)\}$.

6. (Previously Presented) The method of claim 5, wherein said second error-corrected experiment profile $A"_m$ is calculated according to the equation

$$A"_m(k) = (1-w(k)) \cdot A_m(k) + w(k) \cdot A'_m(k).$$

7. (Previously Presented) The method of claim 6, further comprising determining said weighing factor *w(k)* according to the equation

$$w(k) = 1 - e^{-0.5\left[\frac{\bar{c}(k)}{avg\_bkgstd}\right]^2}$$

where *avg_bkgstd* is an average background standard error.

8. (Previously Presented) The method of claim 7, further comprising

determining said *avg_bkgstd* according to the equation

$$avg\_bkgstd = \frac{1}{N}\sum_{k=1}^{N}\left[\frac{1}{M}\sum_{m=1}^{M} bkgstd(m,k)\right]$$

where *bkgstd (m, k)* is background standard error of $C_m(k)$.

9. (Previously Presented) The method of claim 4, further comprising determining errors $\{\sigma'_m(k)\}$ of said data set $\{A'_m(k)\}$ in said first error-corrected experiment profile A'_m.

10. (Previously Presented) The method of claim 9, further comprising determining said errors $\{\sigma'_m(k)\}$ according to the equation

$$\sigma'_m(k) = \sqrt{\sigma_m^2(k) + mixed\_\sigma_m^2(k) - 2 \cdot Cor(k) \cdot \sigma_m(k) \cdot mixed\_\sigma_m(k)}$$

where $\sigma_m(k)$ is the standard error of $A_m(k)$, the method further comprising determining $mixed\_\sigma_m(k)$ according to the equation

$$mixed\_\sigma_m(k) = \frac{\sigma_m(k) + (M-1)\cdot\sigma_{ref}(k)}{M}$$

where $\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_{m}^{M}(C_m(k) - \bar{C}(k))^2}$

and where Cor(k) is a correlation coefficient between said experiment profile A_m and said reference profile C_m.

11. (Previously Presented) The method of claim 10, further comprising determining said Cor(k) according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5 \cdot \left[\frac{\overline{C}(k)}{avg\_bkgstd}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

12. (Previously Presented) The method of claim 7, further comprising determining errors $\{\sigma''_m(k)\}$ of said data set $\{A''_m(k)\}$ in said second error-corrected experiment profile A''_m.

13. (Previously Presented) The method of claim 12, wherein said errors $\{\sigma''_m(k)\}$ are determined according to the equation

$$\sigma''_m(k) = \sqrt{[1 - w(k)] \cdot \sigma_m^2(k) + w(k)\sigma'^2_m(k)}$$

where $\sigma_m(k)$ is the standard error of $A_m(k)$, the method further comprising (i) determining $\sigma'_m(k)$ according to the equation

$$\sigma'_m(k) = \sqrt{\sigma_m^2(k) + mixed\_\sigma_m^2(k) - 2 \cdot Cor(k) \cdot \sigma_m(k) \cdot mixed\_\sigma_m(k)}, \text{ and}$$

(ii) determining $mixed\_\sigma_m(k)$ according to the equation

$$mixed\_\sigma_m(k) = \frac{\sigma_m(k) + (M-1) \cdot \sigma_{ref}(k)}{M}$$

where $\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_{m}^{M}(c_m(k) - \bar{C}(k))^2}$

and where Cor(k) is a correlation coefficient between said experiment profile A_m and said reference profile C_m.

14. (Previously Presented) The method of claim 13, further comprising determining said Cor(k) according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5\cdot\left[\frac{\bar{c}(k)}{avg\_bkgstd}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

15. (Previously Presented) The method of claim 2, wherein said experiment profile A_m and said reference profile C_m of each said profile pair $\{A_m,C_m\}$ are measured in a two-channel microarray experiment.

16. (Previously Presented) The method of claim 15, wherein said reference profiles $\{C_m\}$, where m = 1, 2, ... , M, are measured with samples labeled with a same label.

17. (Previously Presented) The method of claim 2, wherein at least one of said plurality of pairs of profiles $\{A_m, C_m\}$ is a virtual profile.

18. **(Currently Amended)** The method of claim 1, wherein said plurality of pairs of profiles $\{A_m, C_m\}$ are transformed profiles each comprising **error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents in data set $\{A_m(k)\}$ and data set $\{C_m(k)\}$, respectively; and wherein said data set $\{A_m(k)\}$ is said first data set, and said data set $\{C_m(k)\}$ is said second data set.

19. (Canceled)

20. **(Currently Amended)** The method of claim 1, further comprising:

(a0) removing nonlinearity, prior to said calculating step (a), from measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents to generate said plurality of pairs of profiles $\{A_m, C_m\}$ comprising said experiment profile A_m and reference profile C_m.

21. **(Currently Amended)** The method of claim 20, wherein said removing step (a0) comprises:

(a0i) calculating an average profile of pre-experiment profiles $\{A_m^{pre}\}$ and pre- reference profiles $\{C_m^{pre}\}$; wherein each of said pre-experiment profiles comprises measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular

constituents measured in said sample having been subject to said first condition, which when nonlinearity is removed therefrom, produces each said experiment profile A_m; and wherein each of said pre-reference profiles comprises measurements, **error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents measured in said sample having been subject to said second condition, which when nonlinearity is removed therefrom, produces each said reference profile C_m; and

(a0ii) **calculating first differences between each of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile; calculating second differences between each of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile;** adjusting, **wherein the adjusting comprises correcting nonlinearity,** each of said pre-experiment profiles $\{A_m^{pre}\}$ based on **said** first differences between each of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile, thereby generating each said experiment profile A_m; and adjusting, **wherein the adjusting comprises correcting nonlinearity,** each of pre-reference profiles $\{C_m^{pre}\}$ based on **said** second differences between each of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile, thereby generating each said reference profile C_m.

22. **(Currently Amended)** The method of claim 21, further comprising calculating said first differences based on a first subset of said measurements, **error-**

model-based transformed measurements, or **logarithm-based** transformed measurements of said plurality of different cellular constituents in said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile; and calculating said second differences based on a second subset of said measurements, **error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents in said pre-reference profiles $\{C_m^{pre}\}$ and said average profile.

23. **(Currently Amended)** The method of claim 22, wherein said first subset consists of measurements, **error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents that are ranked similarly between each of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile, and said second subset consists of measurements, **error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents that are ranked similarly between each of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile.

24. **(Currently Amended)** The method of claim 23, wherein said adjusting step (a0ii) is carried out by a method comprising:

(ii1) binning said first subset into a first plurality of bins, wherein each of

said first plurality of bins consists of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents in one of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile having a value in a given range; and binning said second subset into a second plurality of bins, wherein each of said second plurality of bins consists of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents in one of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile having a value in a given range;

(ii2) calculating, in each bin of said first plurality of bins, a first mean difference between a feature value of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said one of said pre-experiment profiles $\{A_m^{pre}\}$ and a feature value of said average profile, and calculating a second mean difference between a feature value of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said one of said pre-reference profiles $\{C_m^{pre}\}$ and a feature value of said average profile;

(ii3) determining a first curve of said first mean difference as a first function of values of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular

constituents for said one of said pre-experiment profiles $\{A_m^{pre}\}$,wherein said first function is represented by, $nonlinear\_A_m^{pre}$; and determining a second curve of said second mean difference as a second function of values of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents for said one of said pre-reference profiles $\{C_m^{pre}\}$,wherein said second function is represented by $nonlinear\_C_m^{pre}$; and

(ii4) adjusting each of said pre-experiment profiles $\{A_m^{pre}\}$ according to the equation:

$$A_m(k) = A_m^{pre}(k) - nonlinear\_A_m^{pre}(k),$$

and adjusting each of said pre-reference profiles $\{C_m^{pre}\}$ according to the equation:

$$C_m(k) = C_m^{pre}(k) - nonlinear\_C_m^{pre}(k),$$

where k = 1, ... , N; and where $A_m^{pre}(k)$ and $C_m^{pre}(k)$ are data sets of each of said pre-experiment profiles $\{A_m^{pre}\}$and each of said pre-reference profiles $\{C_m^{pre}\}$, respectively; and where $A_m(k)$ and $C_m(k)$ are said first data set and said second data set, respectively.

25. **(Currently Amended)** The method of claim 1, further comprising:

(a0) normalizing, prior to said calculating step (a), measurements**, error-**

model-based transformed measurements, or **logarithm-based** transformed measurements of said plurality of different cellular constituents in a pre-experiment profile A_m^{pre} and a pre-reference profile C_m^{pre} to generate said experiment profile A_m and said reference profile C_m, respectively.

26. **(Currently Amended)** The method of claim 25, wherein said normalizing step (a0) comprises normalizing a data set $A_m^{pre}(k)$ and a data set $C_m^{pre}(k)$, according to the equations:

$$A_m(k) = \frac{A_m^{pre}(k) - \overline{A_m^{pre}}}{\overline{A_m^{pre}}}$$

and

$$C_m(k) = \frac{C_m^{pre}(k) - \overline{A_m^{pre}}}{\overline{C_m^{pre}}},$$

wherein said data sets $A_m^{pre}(k)$ and $C_m^{pre}(k)$ each comprises measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents, where $\overline{A_m^{pre}}$ is an average of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents in said $A_m^{pre}(k)$, and $\overline{C_m^{pre}}$ is an average of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents in said $C_m^{pre}(k)$, wherein $A_m(k)$ is said

first data set, wherein $A_m(k)$ comprises normalized measurements or normalized transformed measurements of said pre-experiment profile A_m^{pre}; and $C_m(k)$ is said second data set wherein $A_m(k)$ comprises normalized measurements or normalized transformed measurements of said reference profile C_m^{pre}; and wherein $\overline{A_m^{pre}\,C_m^{pre}}$ is an average calculated according to the equation

$$\overline{A_m^{pre}\,C_m^{pre}} = \frac{1}{2M}\sum_{m=1}^{M}(\overline{A_m^{pre}} + \overline{C_m^{pre}}).$$

27. (Previously Presented) The method of claim 26, further comprising normalizing errors of said data sets $\{ A_m^{pre}(k) \}$ and $\{ C_m^{pre}(k) \}$, respectively, according to the equations:

$$\sigma_m^{NA}(k) = \frac{\sigma_m^{preA}(k)\cdot\overline{A_m^{pre}\,C_m^{pre}}}{\overline{A_m^{pre}}}$$

and

$$\sigma_m^{NC}(k) = \frac{\sigma_m^{preC}(k)\cdot\overline{A_m^{pre}\,C_m^{pre}}}{\overline{C_m^{pre}}},$$

where $\sigma_m^{preA}(k)$ and $\sigma_m^{preC}(k)$ are the standard errors of $A_m^{pre}(k)$ and $C_m^{pre}(k)$, respectively, and $\sigma_m^{NA}(k)$ and $\sigma_m^{NC}(k)$ are normalized standard errors of $A_m(k)$ and $C_m(k)$, respectively.

28. (Previously Presented) The method of claim 27, further comprising normalizing background errors of said data sets $\{A_m^{pre}(k)\}$ and $\{C_m^{pre}(k)\}$, respectively, according to the equations:

$$bkgstd_m^{NA}(k) = \frac{bkgstd_m^{preA}(k) \cdot \overline{A_m^{pre}} \, \overline{C_m^{pre}}}{\overline{A_m^{pre}}}$$

and

$$bkgstd_m^{NC}(k) = \frac{bkgstd_m^{preC}(k) \cdot \overline{A_m^{pre}} \, \overline{C_m^{pre}}}{\overline{C_m^{pre}}}$$

where $bkgstd_m^{preA}(k)$ and $bkgstd_m^{preC}(k)$ are the standard background errors of $A_m^{pre}(k)$ and $C_m^{pre}(k)$, respectively, and $bkgstd_m^{NA}(k)$ and $bkgstd_m^{NC}(k)$ are normalized standard background errors of $A_m(k)$ and $C_m(k)$, respectively.

29. **(Currently Amended)** The method of claim 28, further comprising calculating said averages $\overline{A_m^{pre}}$ and $\overline{C_m^{pre}}$ by excluding measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents having a value among the highest 10% of said measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents in said data sets $\{A_m^{pre}(k)\}$ and $\{C_m^{pre}(k)\}$, respectively.

30. **(Currently Amended)** A method for generating at least one error-

corrected experiment profile of at least one experiment profile in a plurality of pairs of profiles $\{XA_m, XC_m\}$, XA_m being an experiment profile, XC_m being a reference profile, where m = 1, 2, ... , M, M is the number of pairs of profiles, said method comprising:

(a) processing, on a suitably programmed computer, said plurality of pairs of profiles $\{XA_m, XC_m\}$ to obtain a plurality of pairs of processed profiles $\{PA_m, PC_m\}$, PA_m being a processed experiment profile, PC_m being a processed reference profile**, wherein said processing comprises normalizing at least one said experiment profile XA_m and reference profile XC_m**;

(b) calculating, on a suitably programmed computer, an average processed reference profile $\overline{PC}$ of processed reference profiles $\{PC_m\}$, where m = 1,2, ..., M;

(c) determining, on a suitably programmed computer, for at least one processed profile pair $\{PA_m, PC_m\}$ where $m \in \{1, 2, ..., M\}$ of said plurality of pairs of processed profiles $\{PA_m, PC_m\}$, where m = 1, 2, ..., M, a differential reference profile computed between PC_m and $\overline{PC}$;

(d) ~~adjusting~~ **via said differential reference profile determined for said at least one processed profile pair, removing**, on a suitably programmed computer, **systematic cross-experiment error from** a processed experiment profile PA_m of said at least one processed profile pair $\{PA_m, PC_m\}$ where $m \in \{1, 2, ..., M\}$ ~~using said differential reference profile determined for said at least one processed profile pair~~ to generate a first error-corrected processed experiment profile PA'_m; wherein

for each m $\in$ {1, 2, ..., M}, said processed experiment profile PA_m comprises a first processed data set, said processed reference profile PC_m comprises a second processed data set, said average processed reference profile $\overline{PC}$ comprises data set $\{\overline{PC}(k)\}$, said first error-corrected processed experiment profile PA'_m comprises dataset $\{PA'_m(k)\}$, said experiment profile XA_m comprises data set $\{XA_m(k)\}$, said reference profile XC_m comprises data set $\{XC_m(k)\}$, wherein said data set $\{XA_m(k)\}$ comprises measurements of a plurality of different cellular constituents measured in a sample having been subject to a first condition, said data set $\{XC_m(k)\}$ comprises measurements of said plurality of different cellular constituents measured in a sample having been subject to a second condition, and where k = 1, 2, ..., N; k is an index of measurements of cellular constituents, N being the total number of measurements;

(e) obtaining a data set $\{PA''_m(k)\}$, wherein obtaining said data set $\{PA''_m(k)\}$ comprises combining said first error-corrected processed experiment profile PA'_m with said processed experiment profile PA_m using a weighing factor $\{w(k)\}$, k = 1 , 2, ..., N, wherein $w(k)$ is a weighing factor for the k'th measurement; and

~~(e)~~ **(f)** outputting to a user, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying: said first error-corrected processed experiment profile PA'_m, said data set$\{PA'_m(k)\}$, a second error-corrected processed experiment profile PA''_m, or **said** data set $\{PA''_m(k)\}$, wherein said second error-corrected processed experiment profile PA''_m comprises

said data set $\{PA''_m(k)\}$ ~~obtained by combining said first error-corrected processed experiment profile PA'_m with said processed experiment profile PA_m using a weighing factor $\{w(k)\}$, k = 1, 2, ..., N, wherein $w(k)$ is a weighing factor for the k'th measurement~~.

31. **(Canceled)**

32. **(Currently Amended)** The method of claim ~~31~~ 30, wherein said normalizing is carried out according to the equations:

$$NA_m(k) = \frac{XA_m(k) \cdot \overline{XAC}}{\overline{XA_m}}$$

and

$$NC_m(k) = \frac{XC_m(k) \cdot \overline{XAC}}{\overline{XC_m}}$$

where $\{NA_m(k)\}$ is said first data set of said processed experiment profile PA_m, and $\{NC_m(k)\}$ is said second data set of said processed reference profile PC_m; where $\overline{XA_m}$ is an average of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents of said data set $\{XA_m(k)\}$, and $\overline{XC_m}$ is an average of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents of data set $\{XC_m(k)\}$; and wherein $\overline{XAC}$ is an average calculated according to the equation

$$\overline{XAC} = \frac{1}{2M} \sum_{m=1}^{M} (\overline{XA_m} + \overline{XC_m}).$$

33. (Previously Presented) The method of claim 32, further comprising normalizing errors of said experiment profile XA_m and reference profile XC_m according to the equations:

$$\sigma_m^A(k) = \frac{\sigma_m^{XA}(k) \cdot \overline{XAC}}{\overline{XA_m}}$$

and

$$\sigma_m^C(k) = \frac{\sigma_m^{XC}(k) \cdot \overline{XAC}}{\overline{XC_m}}$$

where $\sigma_m^{XA}(k)$ and $\sigma_m^{XC}(k)$ are the standard errors of $XA_m(k)$ and $XC_m(k)$, respectively, and $\sigma_m^A(k)$and $\sigma_m^C(k)$ are normalized standard errors of $NA_m(k)$ and $NC_m(k)$, respectively.

34. (Previously Presented) The method of claim 33, further comprising normalizing background errors of said experiment profile XA_m and reference profile XC_m according to the equations:

$$bkgstd_m^A(k) = \frac{bkgstd_m^{XA}(k) \cdot \overline{XAC}}{\overline{XA_m}}$$

and

$$bkgstd\,{}^{C}_{m}(k) = \frac{bkgstd\,{}^{XC}_{m}(k)\cdot\overline{XAC}}{\overline{XC_m}}$$

where $bkgstd\,{}^{XA}_{m}(k)$ and $bkgstd\,{}^{XC}_{m}(k)$ are the standard background errors of $XA_m(k)$ and $XC_m(k)$, respectively, and $bkgstd\,{}^{A}_{m}(k)$ and $bkgstd\,{}^{C}_{m}(k)$ are normalized standard background errors of said $NA_m(k)$ and said $NC_m(k)$, respectively.

35. (**Currently Amended**) The method of claim 33, further comprising determining said averages $\overline{XA_m}$ and $\overline{XC_m}$ excluding measurements of said plurality of different cellular constituents having a value among the highest 10% of said measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents in said data sets $\{XA_m(k)\}$ and $\{XC_m(k)\}$, respectively.

36. (**Currently Amended**) The method of claim 30, wherein said processing step (a) comprises:

normalizing each said experiment profile XA_m and reference profile XC_m to generate normalized data set $\{NA_m(k)\}$ and normalized data set $\{NC_m(k)\}$, respectively;

transforming said normalized data set $\{NA_m(k)\}$ to obtain a transformed data set $\{TA_m(k)\}$, where said transformed data set $\{TA_m(k)\}$ is said first data set of said processed experiment profile PA_m; and

transforming said normalized data set $\{NC_m(k)\}$ to obtain a transformed data set

$\{TC_m(k)\}$, where said transformed data set $\{TC_m(k)\}$ is said second data set of said processed reference profile PC_m;

wherein said transforming is carried out for an experiment according to equations

$$TA_m(k) = f(x) = \frac{1n\left[\frac{b^2+2\cdot a^2\cdot NA_m(k)}{a} + 2\cdot\sqrt{c^2+b^2\cdot NA_m(k)+a^2\cdot[NA_m(k)]^2}\right]}{a} + d_2$$

for $NA_m(k)>0$

and

$$TC_m(k) = f(x) = \frac{1n\left[\frac{b^2+2\cdot a^2\cdot NC_m(k)}{a} + 2\cdot\sqrt{c^2+b^2\cdot NC_m(k)+a^2\cdot[NC_m(k)]^2}\right]}{a} + d_2$$

for $NC_m(k)>0$

where d is described by equation

$$d = \frac{-1n\left[\frac{b^2}{a}+2\cdot c\right]}{a}$$

and where a is the fractional error coefficient of said experiment, b is the Poisson error coefficient of said experiment, and c is the standard deviation of background noise of said experiment.

37. (Canceled)

38. **(Currently Amended)** The method of claim 30, wherein said processing step (a) comprises:

normalizing each said experiment profile XA_m and reference profile XC_m to

generate normalized data set $\{NA_m(k)\}$ and normalized data set $\{NC_m(k)\}$, respectively;

transforming said normalized data set $\{NA_m(k)\}$ **to a new domain in which variance becomes a constant** to obtain a transformed data set $\{TA_m(k)\}$;

transforming said normalized data set $\{NC_m(k)\}$ **to the new domain in which variance becomes a constant** to obtain a transformed data set $\{TC_m(k)\}$; and

removing nonlinearity from each said transformed data sets $\{TA_m(k)\}$ and $\{TC_m(k)\}$, respectively.

39. **(Currently Amended)** The method of claim 38, wherein said removing nonlinearity is carried out by a method comprising

(a1) calculating an average transformed profile of transformed experiment profiles and transformed reference profiles, wherein each of said transformed experiment profiles contains a corresponding transformed data set $\{TA_m(k)\}$, and each of said transformed reference profiles contains a corresponding transformed data set $\{TC_m(k)\}$; and

(a2) **calculating first differences between each of said transformed experiment profiles and said average transformed profile; calculating second differences between each of said transformed reference profiles and said average transformed profile;** adjusting**, wherein the adjusting corrects nonlinearity,** each of said transformed experiment profiles based on **said** first differences between each of said transformed experiment profiles and said average

transformed profile, and adjusting**, wherein the adjusting corrects nonlinearity,** each of said transformed reference profiles based on **said** second differences between each of said transformed reference profiles and said average transformed profile.

40. **(Currently Amended)** The method of claim 39, further comprising calculating said first differences based on the differences in a first subset of **error-model-based transformed measurements or logarithm-based** transformed measurements of said plurality of different cellular constituents between each of said transformed experiment profiles and said average transformed profile, and calculating said second differences based on the differences in a second subset of transformed measurements of said plurality of different cellular constituents between each of said transformed reference profiles and said average transformed profile.

41. **(Currently Amended)** The method of claim 40, wherein each said first subset consists of **error-model-based transformed measurements or logarithm-based** transformed measurements that are ranked similarly between each of said transformed experiment profiles and said average transformed profile, and each said second subset consists of **error-model-based transformed measurements or logarithm-based** transformed measurements that are ranked similarly between each of said transformed reference profiles and said average transformed profile.

42. (**Currently Amended**) The method of claim 41, wherein said adjusting step (a2) is carried out by a method comprising:

(a2i) binning said first subset into a plurality of bins, each said bin consisting of **error-model-based transformed measurements or logarithm-based** transformed measurements of said plurality of different cellular constituents in one of said transformed experiment profiles and said average transformed profile having a value in a given range; and binning said second subset into a plurality of bins, each said bin consisting of **error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents in one of said transformed reference profiles and said average transformed profile having a value in a given range;

(a2ii) calculating, in each bin of said plurality of bins, a first mean difference between a feature value of **error-model-based transformed measurements or logarithm-based** transformed measurements of said plurality of different cellular constituents in said one of said transformed experiment profiles and a feature value of said average transformed profile, and calculating a second mean difference between a feature value of transformed measurements of said plurality of different cellular constituents in said one of said reference profiles and a feature value of the average profile;

(a2iii) determining a first curve of said first mean difference as a first function of values of **error-model-based transformed measurements or logarithm-based** transformed measurements of said plurality of different cellular constituents for said one

of said transformed experiment profiles, wherein said first function is represented by, *nonlinear_TA$_m$,* and determining a second curve of said second mean difference as a second function of values of transformed measurements of said plurality of different cellular constituents for said one of said transformed reference profiles, wherein said second function is represented by *nonlinear_TC$_m$;* and

(a2iv) computing corrected transformed measurements of said plurality of different cellular constituents in each said transformed data set {TA$_m$(k)}, according to the equation:

$$TA_m^{corr}(k) = TA_m(k) - nonlinear\_TA_m(k),$$

and computing corrected transformed measurements of said plurality of different cellular constituents in each said transformed data set {TC$_m$(k)}, according to the equation:

$$TC_m^{corr}(k) = TC_m(k) - nonlinear\_TC_m(k),$$

where k = 1, ..., N; and where $\{TA_m^{corr}(k)\}$ is said first processed data set of said processed experiment profile PA$_m$, and $\{TC_m^{corr}(k)\}$ is said second processed data set of said processed reference profile PC$_m$.

43. (**Currently Amended**) The method of claim 42, wherein said processed experiment profile PA$_m$ and said processed reference profile PC$_m$ comprise **error-model-based transformed measurements or logarithm-based** transformed measurements of said plurality of different cellular constituents from the same experimental reaction.

44. **(Currently Amended)** The method of claim 43, further comprising calculating $\overline{PC}(k)$ according to the equation

$$\overline{PC}(k) = \frac{1}{M} \sum_{m=1}^{M} PC_m(k),$$

wherein $\{PC_m(k)\}$ comprises **error-model-based transformed measurements or logarithm-based** transformed measurements from said second processed data set $\{TC_m^{corr}(k)\}$ and calculating said differential reference profile according to the equation

$$PC_{diff}(m,k) = PC_m(k) - \overline{PC}(k)$$

and wherein said first error-corrected profile is calculated according to the equation

$$PA'_m(k) = PA_m(k) - PC_{diff}(m,k),$$

wherein $\{PA_m(k)\}$ comprises **error-model-based transformed measurements or logarithm-based** transformed measurements from said first data set $\{TA_m^{corr}(k)\}$.

45. (Previously Presented) The method of claim 44, further comprising

(d) calculating for each processed profile pair $\{PA_m, PC_m\}$, where $m \in \{1, 2, ..., M\}$, a second error-corrected experiment profile PA''_m comprising data set $\{PA''_m(k)\}$ by combining said first error-corrected experiment profile PA'_m with said processed experiment profile PA_m using a weighing factor $\{w(k)\}$, k = 1,2, ..., N, wherein $w(k)$ is a weighing factor for the k'th measurement.

46. (Previously Presented) The method of claim 45, wherein said second error-corrected experiment profile PA''_m is calculated according to the equation

$$PA''_m(k) = (1\text{-}w(k)) \cdot PA_m(k) + w(k)PA'_m(k).$$

47. (Previously Presented) The method of claim 46, further comprising determining said weighing factor according to the equation

$$w(k) = 1\text{-}e^{-0.5\left[\frac{\overline{PC}(k)}{avg\_bkgstd}\right]^2}$$

where *avg_bkgstd* is an average background standard error.

48. (Previously Presented) The method of claim 47, further comprising determining said *avg_ bkgstd* according to the equation

$$avg\_bkgstd = \frac{1}{N}\sum_{k=1}^{N}\left[\frac{1}{M}\sum_{m=1}^{M} bkgstd(m,k)\right]$$

where *bkgstd (m, k)* is background standard error of $PC_m(k)$.

49. (Previously Presented) The method of claim 44, further comprising determining errors $\{P\sigma'_m\}$ of said first error-corrected experiment profile $\{PA'_m\}$, wherein said $\{P\sigma'_m\}$ comprises error data set $\{P\sigma'_m(k)\}$.

50. (Previously Presented) The method of claim 49, further comprising determining said error data set $\{P\sigma'_m(k)\}$ according to the equation

$$\sigma'_m(k) = \sqrt{P\sigma'^2_m(k) = mixed\_P\sigma_m{}^2(k) - 2Cor(k) \cdot P\sigma_m(k) \cdot mixed\_P\sigma_m(k)}$$

where $P\sigma_m(k)$ is the standard error of $A_m(k)$, and determining $mixed\_P\sigma_m(k)$ according to the equation

$$mixed\_P\sigma_m(k) = \frac{P\sigma_m(k) + (M-1) \cdot P\sigma_{ref}(k)}{M}$$

where

$$P\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_{m}^{M} (PC_m(k) - \overline{PC}(k))^2}$$

and where Cor(k) is a correlation coefficient between said processed experiment profile PA_m and said processed reference profile PC_m.

51. (Previously Presented) The method of claim 50, wherein said Cor(k) is determined according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5\left[\frac{\overline{PC}(k)}{avg\_bkgstd}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

52. (Previously Presented) The method of claim 51, further comprising determining errors $\{P\sigma''_m\}$ of said second error-corrected experiment profile $\{PA''_m\}$ wherein said $\{P\sigma''_m\}$ comprises error data set $\{P\sigma''_m(k)\}$.

53. (Previously Presented) The method of claim 52, further comprising determining said error data set $\{P\sigma''_m(k)\}$ according to the equation

$$P\sigma''_m(k) = \sqrt{[1 - w(k)] \cdot P\sigma_m^2(k) + w(k)P\sigma'^2_m(k)}$$

where $P\sigma_m(k)$ is the standard error of $PA_m(k)$, and further comprising determining $P\sigma'_m(k)$ according to the equation

$$P\sigma'_m(k) = \sqrt{P\sigma_m^2(k) + mixed\_P\sigma_m^2(k) - 2 \cdot Cor(k) \cdot P\sigma_m(k) \cdot mixed\_P\sigma_m(k)},$$

and

further comprising determining $mixed\_P\sigma_m(k)$ according to the equation

$$mixed\_P\sigma_m(k) = \frac{P\sigma_m(k) + (M-1) \cdot P\sigma_{ref}(k)}{M}$$

where

$$P\sigma_{ref}(k) = \sqrt{\frac{1}{M-1} \sum_{m}^{M} (PC_m(k) - \overline{PC}(k))^2}$$

and where Cor(k) is a correlation coefficient between said processed experiment profile PA_m and said processed reference profile PC_m.

54. (Previously Presented) The method of claim 53, further comprising determining said Cor(k) according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5\left[\frac{\overline{PC}(k)}{avg\_bkgstd}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

55. (Previously Presented) The method of claim 54, wherein each said pair of profiles XA_m and XC_m comprise measurements of said plurality of different cellular constituents from a two-channel microarray experiment.

56. (Previously Presented) The method of claim 55, wherein said reference profiles $\{XC_m\}$, m = 1, 2, ... , M, are measured with samples labeled with a same label.

57. (Previously Presented) The method of claim 56, wherein at least one of said pairs of profiles $\{XA_m, XC_m\}$ is a virtual profile.

58. (Canceled)

59. (Canceled)

60. (Canceled)

61. (Canceled)

62. (Canceled)

63. (Canceled)

64. (Canceled)

65. (Canceled)

66. **(Currently Amended)** A method for generating at least one error-corrected experiment profile of at least one experiment profile A_m, where $m \in \{1, 2, ..., M\}$ in at least one of a plurality of pairs of profiles $\{A_m, C_m\}$, A_m being an experiment profile, C_m being a reference profile, where $m = 1, 2, ..., M$, M is the number of pairs of profiles, said method comprising:

~~adjusting~~ **via a differential reference profile calculated between C_m and an average reference profile $\bar{C}$, removing**, on a suitably programmed computer, **systematic cross-experiment error from** said experiment profile A_m ~~using a differential reference profile calculated between C_m and an average reference profile $\bar{C}$ determined~~ for profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, ..., M\}$ to generate a first error-corrected experiment profile A'_m; wherein said average reference profile $\bar{C}$ is an average of reference profiles $\{C_m\}$, $m = 1, 2, ..., M$; wherein for each $m \in \{1, 2, ..., M\}$, said first error-corrected experiment profile A'_m comprises data set $\{A'_m(k)\}$, said experiment profile A_m comprises data set $\{A_m(k)\}$, said reference profile C_m comprises data set $\{C_m(k)\}$, and said average reference profile $\bar{C}$ comprises data set $\{\bar{C}(k)\}$, wherein said data set $\{A_m(k)\}$ comprises measurements, **error-model-based transformed measurements,** or **logarithm-based** transformed measurements of a plurality of different cellular constituents measured in a sample having been subject to a first condition, said data set $\{C_m(k)\}$ comprises

measurements, **error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents measured in a sample having been subject to a second condition, wherein k = 1, 2, ... , N; k is an index of measurements, **error-model-based transformed measurements,** or **logarithm-based** transformed measurements of cellular constituents, N being the total number of measurements;

obtaining a data set $\{A"_m(k)\}$, wherein obtaining said data set $\{A"_m(k)\}$ comprises combining said first error-corrected experiment profile A'_m with said experiment profile A_m using a weighing factor $\{w(k)\}$, k = 1, 2, ... , N, wherein $w(k)$ is a weighing factor for the k'th measurement; and

outputting to a user, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying: said first error-corrected experiment profile A'_m, said data set $\{A'_m(k)\}$, a second error-corrected experiment profile $A"_m$, or ~~a~~ **said** data set $\{A"_m(k)\}$, wherein said second error-corrected experiment profile $A"_m$ comprises said data set $\{A"_m(k)\}$ ~~**obtained by combining said first error-corrected experiment profile A'_m with said experiment profile A_m using a weighing factor $\{w(k)\}$, k = 1, 2, ... , N, wherein $w(k)$ is a weighing factor for the k'th measurement**~~.

67. (Previously Presented) The method of claim 18, further comprising obtaining said transformed measurements of said data set $\{A_m(k)\}$ and said data set $\{C_m(k)\}$ for an experiment according to the equations:

$$A_m(k) = f(x) = \frac{1n\left[\frac{b^2+2\cdot a^2\cdot XA_m(k)}{a} + 2\cdot\sqrt{c^2+b^2\cdot XA_m(k)+a^2\cdot[XA_m(k)]^2}\right]}{a} + d,$$

for $XA_m(k)>0$

and

$$C_m(k) = f(x) = \frac{1n\left[\frac{b^2+2\cdot a^2\cdot XC_m(k)}{a} + 2\cdot\sqrt{c^2+b^2\cdot XC_m(k)+a^2\cdot[XC_m(k)]^2}\right]}{a} + d,$$

for $XC_m(k)>0$

where $\{XA_m(k)\}$ and $\{XC_m(k)\}$ are data sets comprising measurements of said plurality of different cellular constituents that when transformed produce said transformed measurements of said plurality of different cellular constituents of said data set $A_m(k)$ and said data set $C_m(k)$, respectively, where d is described by the equation:

$$d = \frac{-1n\left[\frac{b^2}{a}+2\cdot c\right]}{a}$$

and where a is the fractional error coefficient of said experiment, b is the Poisson error coefficient of said experiment, and c is the standard deviation of background noise of said experiment.

68. (Canceled)

69. (Canceled)

70. (Previously Presented) The method of claim 30, wherein said processing comprises:

normalizing, transforming, and/or removing nonlinearity from measurements of said plurality of cellular constituents of said data set $\{XA_m(k)\}$ of said experiment profile XA_m, and from measurements of said plurality of cellular constituents of said data set $\{XC_m(k)\}$ of said reference profile XC_m.

71. (**Currently Amended**) A computer program product for use in conjunction with a computer having a processor and a memory connected to the processor, said computer program product comprising a computer readable storage medium having a computer program mechanism encoded thereon, wherein said computer program mechanism may be loaded into the memory of said computer and cause said computer to carry out a method for generating at least one error-corrected experiment profile of at least one experiment profile in a plurality of pairs of profiles $\{A_m,C_m\}$, where m = 1,2, …, M, and M is the number of the pairs of profiles; and wherein, for each m ϵ {1, 2, …, M}, A_m is an experiment profile, and C_m is a reference profile; and wherein $\{A_m\}$ represents experiment profiles in said plurality of pairs of profiles $\{A_m,C_m\}$ and $\{C_m\}$ represents reference profiles in said plurality of pairs of profiles $\{A_m, C_m\}$, said method comprising:

(a) calculating, on a computer, an average reference profile $\bar{C}$ of said plurality of reference profiles $\{C_m\}$ where m = 1, 2, …, M;

(b) determining, on a computer, for at least one profile pair $\{A_m,C_m\}$ where m ϵ

{1, 2, …, M} of said plurality of pairs of profiles $\{A_m, C_m\}$ a differential reference profile computed between C_m and $\bar{C}$;

(c) ~~adjusting~~ **via said differential reference profile determined for said profile pair, removing**, on a computer, **systematic cross-experiment error from** an experiment profile A_m of said at least one profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, \ldots, M\}$ ~~based on said differential reference profile determined for said profile pair~~ to generate a first error-corrected experiment profile A'_m for each $m \in \{1, 2, \ldots, M\}$, wherein said experiment profile A_m comprises a first data set, said reference profile C_m comprises a second data set, said average reference profile $\bar{C}$ comprises data set $\{\bar{C}(k)\}$, and said first error-corrected experiment profile A'_m comprises data set $\{A'_m(k)\}$; wherein said first data set comprises measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of a plurality of different cellular constituents measured in a sample having been subject to a first condition, said second data set comprises measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents measured in a sample having been subject to a second condition; and wherein k = 1, 2, ..., N; k is an index of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents, N being the total number of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements;

(d) obtaining a data set $\{A''_m(k)\}$ by combining said first error-corrected

experiment profile A'_m with said experiment profile A_m using a weighing factor $\{w(k)\}$, k = 1, 2, ... , N, wherein *w(k)* is a weighing factor for the *k*'th measurement; and

~~(d)~~ **(e)** outputting to a user, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying: said first error-corrected experiment profile A'_m, said data set $\{A'_m(k)\}$, a second error-corrected experiment profile $A"_m$, or ~~a~~ **said** data set $\{A"_m(k)\}$, wherein said second error-corrected experiment profile $A"_m$ comprises said data set $\{A"_m(k)\}$ ~~obtained by combining said first error-corrected experiment profile A'_m with said experiment profile A_m using a weighing factor $\{w(k)\}$, k = 1, 2, ... , N, wherein $w(k)$ is a weighing factor for the k'th measurement~~.

72. (Previously Presented) The computer program product of claim 71, wherein said steps (b) and (c) are performed for each profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, ... , M\}$.

73. **(Currently Amended)** The computer program product of claim 72, wherein each of said experiment profile A_m and said reference profile C_m comprises measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents from the same experimental reaction.

74. (Previously Presented) The computer program product of claim 73, wherein said $\bar{C}(k)$ is calculated according to the equation

$$\bar{C}(k) = \frac{1}{M}\sum_{m=1}^{M} C_m(k)$$

wherein said differential reference profile is determined according to the equation

$$C_{diff}(m,k) = C_m(k) - \bar{C}(k)$$

and wherein said first error-corrected experiment profile A'_m is generated according to the equation

$$A'_m(k) = A_m(k) - C_{diff}(m,k)$$

wherein $\{A_m(k)\}$ is said first data set of experiment profile A_m.

75. (**Currently Amended**) The computer program product of claim 74, wherein the method further comprises:

(d) calculating, for **one or more remaining profile pairs out of** ~~each said~~ **said** profile ~~pair~~ **pairs** $\{A_m, C_m\}$, ~~said~~ **a respective** second error-corrected experiment profile $A"_m$; and

(e) outputting to, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying; said **respective** second error-corrected experiment profile $A"_m$ or said data set $\{A"_m(k)\}$.

76. (Previously Presented) The computer program product of claim 75, wherein said second error-corrected experiment profile $A"_m$ is calculated according to the equation

$$A"_m(k) = (1\text{-}w(k)) \cdot A_m(k) + w(k) \cdot A'_m(k).$$

77. (Previously Presented) The computer program product of claim 76, wherein the method further comprises determining said weighing factor *w(k)* according to the equation

$$w(k) = 1 - e^{-0.5\left[\frac{\bar{c}(k)}{avg\_bkgstd}\right]^2}$$

where *avg_bkgstd* is an average background standard error.

78. (Previously Presented) The computer program product of claim 77, wherein the method further comprises determining said *avg_bkgstd* according to the equation

$$avg\_bkgstd = \frac{1}{N}\sum_{k=1}^{N}\left[\frac{1}{M}\sum_{m=1}^{M} bkgstd(m,k)\right]$$

where *bkgstd (m, k)* is background standard error of $C_m(k)$.

79. (Previously Presented) The computer program product of claim 74, wherein the method further comprises determining errors $\{\sigma'_m(k)\}$ of said data set $\{A'_m(k)\}$ in said first error-corrected experiment profile A'_m.

80. (Previously Presented) The computer program product of claim 79, wherein the method further comprises determining said errors $\{\sigma'_m(k)\}$ according to the equation

$$\sigma'_m(k) = \sqrt{\sigma_m^2(k) + mixed\_\sigma_m^2(k) - 2 \cdot Cor(k) \cdot \sigma_m(k) \cdot mixed\_\sigma_m(k)}$$

where $\sigma_m(k)$ is the standard error of $A_m(k)$, the method further comprising determining $mixed\_\sigma_m(k)$ according to the equation

$$mixed\_\sigma_m(k) = \frac{\sigma_m(k) + (M-1)\cdot\sigma_{ref}(k)}{M}$$

where $\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_{m}^{M}(C_m(k) - \bar{C}(k))^2}$

and where Cor(k) is a correlation coefficient between said experiment profile A_m and said reference profile C_m.

81. (Previously Presented) The computer program product of claim 80, wherein the method further comprises determining said Cor(k) according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5 \cdot \left[\frac{\bar{C}(k)}{avg\_bkgstd}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

82. (Previously Presented) The computer program product of claim 77,

wherein the method further comprises determining errors $\{\sigma''_m(k)\}$ of said data set $\{A''_m(k)\}$ in said second error-corrected experiment profile A''_m.

83. (Previously Presented) The computer program product of claim 82, wherein said errors $\{\sigma''_m(k)\}$ are determined according to the equation

$$\sigma''_m(k) = \sqrt{[1 - w(k)] \cdot \sigma_m^2(k) + w(k)\sigma'^2_m(k)}$$

where $\sigma_m(k)$ is the standard error of $A_m(k)$, the method further comprising (i) determining $\sigma'_m(k)$ according to the equation

$$\sigma'_m(k) = \sqrt{\sigma^2_m(k) + mixed\_\sigma_m^2(k) - 2 \cdot Cor(k) \cdot \sigma_m(k) \cdot mixed\_\sigma_m(k)}, \text{ and}$$

(ii) determining $mixed\_\sigma_m(k)$ according to the equation

$$mixed\_\sigma_m(k) = \frac{\sigma_m(k) + (M-1) \cdot \sigma_{ref}(k)}{M}$$

where $\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_m^M (c_m(k) - \bar{C}(k))^2}$

and where Cor(k) is a correlation coefficient between said experiment profile A_m and said reference profile C_m.

84. (Previously Presented) The computer program product of claim 83, wherein the method further comprises determining said Cor(k) according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5\left[\frac{\bar{c}(k)}{avg\_bkgstd}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

85. (Previously Presented) The computer program product of claim 72, wherein said experiment profile A_m and said reference profile C_m of each said profile pair $\{A_m, C_m\}$ are measured in a two-channel microarray experiment.

86. (Previously Presented) The computer program product of claim 85, wherein said reference profiles $\{C_m\}$, where m = 1, 2, ... , M, are measured with samples labeled with a same label.

87. (Previously Presented) The computer program product of claim 72, wherein at least one of said plurality of pairs of profiles $\{A_m, C_m\}$ is a virtual profile.

88. **(Currently Amended)** The computer program product of claim 71, wherein said plurality of pairs of profiles $\{A_m, C_m\}$ are transformed profiles each comprising **error-model-based transformed measurements or logarithm-based** transformed measurements of said plurality of different cellular constituents in data set $\{A_m(k)\}$ and data set $\{C_m(k)\}$, respectively; and wherein said data set $\{A_m(k)\}$ is said first data set, and said data set $\{C_m(k)\}$ is said second data set.

89. **(Currently Amended)** The computer program product of claim 71, wherein the method further comprises:

(a0) removing nonlinearity, prior to said calculating step (a), from measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents to generate said plurality of pairs of profiles $\{A_m, C_m\}$ comprising said experiment profile A_m and reference profile C_m.

90. **(Currently Amended)** The computer program product of claim 89, wherein said removing step (a0) comprises:

(a0i) calculating an average profile of pre-experiment profiles $\{A_m^{pre}\}$ and pre- reference profiles $\{C_m^{pre}\}$; wherein each of said pre-experiment profiles comprises measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents measured in said sample having been subject to said first condition, which when nonlinearity is removed therefrom, produces each said experiment profile A_m; and wherein each of said pre-reference profiles comprises measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents measured in said sample having been subject to said second condition, which when nonlinearity is removed therefrom, produces each said reference profile C_m; and

(a0ii) **calculating first differences between each of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile; calculating second differences between each of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile;** adjusting**, wherein the adjusting comprises correcting nonlinearity,** each of said pre-experiment profiles $\{A_m^{pre}\}$ based on **said** first differences between each of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile, thereby generating each said experiment profile A_m; and adjusting**, wherein the adjusting comprises correcting nonlinearity,** each of pre-reference profiles $\{C_m^{pre}\}$ based on **said** second differences between each of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile, thereby generating each said reference profile C_m.

91. **(Currently Amended)** The computer program product of claim 90, wherein the method further comprises calculating said first differences based on a first subset of said measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents in said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile; and calculating said second differences based on a second subset of said measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents in said pre-reference

profiles $\{C_m^{pre}\}$ and said average profile.

92. **(Currently Amended)** The computer program product of claim 91, wherein said first subset consists of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents that are ranked similarly between each of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile, and said second subset consists of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents that are ranked similarly between each of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile.

93. **(Currently Amended)** The computer program product of claim 92, wherein said adjusting step (a0ii) is carried out by a method comprising:

(ii1) binning said first subset into a first plurality of bins, wherein each of said first plurality of bins consists of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents in one of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile having a value in a given range; and binning said second subset into a second plurality of bins, wherein each of said second plurality of bins consists of measurements**, error-model-based transformed measurements,** or **logarithm-**

based transformed measurements of said plurality of different cellular constituents in one of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile having a value in a given range;

(ii2) calculating, in each bin of said first plurality of bins, a first mean difference between a feature value of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said one of said pre-experiment profiles $\{A_m^{pre}\}$ and a feature value of said average profile, and calculating a second mean difference between a feature value of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said one of said pre-reference profiles $\{C_m^{pre}\}$ and a feature value of said average profile;

(ii3) determining a first curve of said first mean difference as a first function of values of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents for said one of said pre-experiment profiles $\{A_m^{pre}\}$, wherein said first function is represented by, $nonlinear\_A_m^{pre}$; and determining a second curve of said second mean difference as a second function of values of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents for said one of said pre-reference profiles $\{C_m^{pre}\}$, wherein said second function is represented by

$nonlinear\_C_m^{pre}$; and

(ii4) adjusting each of said pre-experiment profiles $\{A_m^{pre}\}$ according to the equation:

$$A_m(k) = A_m^{pre}(k) - nonlinear\_A_m^{pre}(k),$$

and adjusting each of said pre-reference profiles $\{C_m^{pre}\}$ according to the equation:

$$C_m(k) = C_m^{pre}(k) - nonlinear\_C_m^{pre}(k),$$

where k = 1, ... , N; and where $A_m^{pre}(k)$ and $C_m^{pre}(k)$ are data sets of each of said pre-experiment profiles $\{A_m^{pre}\}$ and each of said pre-reference profiles $\{C_m^{pre}\}$, respectively; and where $A_m(k)$ and $C_m(k)$ are said first data set and said second data set, respectively.

94. **(Currently Amended)** The computer program product of claim 71, wherein the method further comprises:

(a0) normalizing, prior to said calculating step (a), measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents in a pre-experiment profile A_m^{pre} and a pre-reference profile C_m^{pre} to generate said experiment profile A_m and said reference profile C_m, respectively.

95. **(Currently Amended)** The computer program product of claim 94,

wherein said normalizing step (a0) comprises normalizing a data set $A_m^{pre}(k)$ and a data set $C_m^{pre}(k)$, according to the equations:

$$A_m(k) = \frac{A_m^{pre}(k) - \overline{A_m^{pre}}\,\overline{C_m^{pre}}}{\overline{A_m^{pre}}}$$

and

$$C_m(k) = \frac{C_m^{pre}(k) - \overline{A_m^{pre}}\,\overline{C_m^{pre}}}{\overline{C_m^{pre}}},$$

wherein said data sets $A_m^{pre}(k)$ and $C_m^{pre}(k)$ each comprises measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents, where $\overline{A_m^{pre}}$ is an average of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents in said $A_m^{pre}(k)$, and $\overline{C_m^{pre}}$ is an average of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents in said $C_m^{pre}(k)$, wherein $A_m(k)$ is said first data set, wherein $A_m(k)$ comprises normalized measurements or normalized transformed measurements of said pre-experiment profile A_m^{pre}; and $C_m(k)$ is said second data set wherein $A_m(k)$ comprises normalized measurements or normalized transformed measurements of said reference profile C_m^{pre}; and wherein $\overline{A_m^{pre}}\,\overline{C_m^{pre}}$ is an average calculated according to the equation

$$\overline{A_m^{pre} C_m^{pre}} = \frac{1}{2M} \sum_{m=1}^{M} (\overline{A_m^{pre}} + \overline{C_m^{pre}}).$$

96. (Previously Presented) The computer program product of claim 95, wherein the method further comprises normalizing errors of said data sets { $A_m^{pre}(k)$ } and { $C_m^{pre}(k)$ }, respectively, according to the equations:

$$\sigma_m^{NA}(k) = \frac{\sigma_m^{preA}(k) \cdot \overline{A_m^{pre} C_m^{pre}}}{\overline{A_m^{pre}}}$$

and

$$\sigma_m^{NC}(k) = \frac{\sigma_m^{preC}(k) \cdot \overline{A_m^{pre} C_m^{pre}}}{\overline{C_m^{pre}}},$$

where $\sigma_m^{preA}(k)$ and $\sigma_m^{preC}(k)$ are the standard errors of $A_m^{pre}(k)$ and $C_m^{pre}(k)$, respectively, and $\sigma_m^{NA}(k)$ and $\sigma_m^{NC}(k)$ are normalized standard errors of $A_m(k)$ and $C_m(k)$, respectively.

97. (Previously Presented) The computer program product of claim 96, wherein the method further comprises normalizing background errors of said data sets $\{A_m^{pre}(k)\}$ and $\{C_m^{pre}(k)\}$, respectively, according to the equations:

$$bkgstd_m^{NA}(k) = \frac{bkgstd_m^{preA}(k) \cdot \overline{A_m^{pre} C_m^{pre}}}{\overline{A_m^{pre}}}$$

and

$$bkgstd_m^{NC}(k) = \frac{bkgstd_m^{preC}(k) \cdot \overline{A_m^{pre}} \overline{C_m^{pre}}}{\overline{C_m^{pre}}}$$

where $bkgstd_m^{preA}(k)$ and $bkgstd_m^{preC}(k)$ are the standard background errors of $A_m^{pre}(k)$ and $C_m^{pre}(k)$, respectively, and $bkgstd_m^{NA}(k)$ and $bkgstd_m^{NC}(k)$ are normalized standard background errors of $A_m(k)$ and $C_m(k)$, respectively.

98. (**Currently Amended**) The computer program product of claim 97, wherein the method further comprises calculating said averages $\overline{A_m^{pre}}$ and $\overline{C_m^{pre}}$ by excluding measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents having a value among the highest 10% of said measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents in said data sets $\{A_m^{pre}(k)\}$ and $\{C_m^{pre}(k)\}$, respectively.

99. (**Currently Amended**) A computer program product for use in conjunction with a computer having a processor and a memory connected to the processor, said computer program product comprising a computer readable storage medium having a computer program mechanism encoded thereon, wherein said computer program mechanism may be loaded into the memory of said computer and cause said computer to carry out a method for generating at least one error-corrected

experiment profile of at least one experiment profile in a plurality of pairs of profiles $\{XA_m, XC_m\}$, XA_m being an experiment profile, XC_m being a reference profile, where m = 1, 2, ... , M, M is the number of pairs of profiles, said method comprising:

(a) processing, on a computer, said plurality of pairs of profiles $\{XA_m, XC_m\}$ to obtain a plurality of pairs of processed profiles $\{PA_m, PC_m\}$, PA_m being a processed experiment profile, PC_m being a processed reference profile, **wherein said processing comprises normalizing at least one said experiment profile XA_m and reference profile XC_m**;

(b) calculating, on a computer, an average processed reference profile $\overline{PC}$ of processed reference profiles $\{PC_m\}$, where m = 1,2, ..., M;

(c) determining, on a computer, for at least one processed profile pair $\{PA_m, PC_m\}$ where $m \in \{1, 2, ..., M\}$ of said plurality of pairs of processed profiles $\{PA_m, PC_m\}$, where m = 1, 2, ..., M, a differential reference profile computed between PC_m and $\overline{PC}$;

(d) ~~adjusting~~ **via said differential reference profile determined for said at least one processed profile pair, removing**, on a computer, **systematic cross-experiment error from** a processed experiment profile PA_m of said at least one processed profile pair $\{PA_m, PC_m\}$ where $m \in \{1, 2, ..., M\}$ ~~using said differential reference profile determined for said at least one processed profile pair~~ to generate a first error-corrected processed experiment profile PA'_m ; wherein for each

$m \in \{1, 2, ..., M\}$, said processed experiment profile PA_m comprises a first processed data set, said processed reference profile PC_m comprises a second processed data set, said average processed reference profile $\overline{PC}$ comprises data set $\{\overline{PC}(k)\}$, said first error-corrected processed experiment profile PA'_m comprises dataset $\{PA'_m(k)\}$, said experiment profile XA_m comprises data set $\{XA_m(k)\}$, said reference profile XC_m comprises data set $\{XC_m(k)\}$, wherein said data set $\{XA_m(k)\}$ comprises measurements of a plurality of different cellular constituents measured in a sample having been subject to a first condition, said data set $\{XC_m(k)\}$ comprises measurements of said plurality of different cellular constituents measured in a sample having been subject to a second condition, and where $k = 1, 2, ..., N$; k is an index of measurements of cellular constituents, N being the total number of measurements;

(e) obtaining data set $\{PA''_m(k)\}$, wherein obtaining said data set $\{PA''_m(k)\}$ comprises combining said first error-corrected processed experiment profile PA'_m with said processed experiment profile PA_m using a weighing factor $\{w(k)\}$, $k = 1, 2, ..., N$, wherein $w(k)$ is a weighing factor for a k'th measurement; and

~~(e)~~ **(f)** outputting to a user, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying: said first error-corrected processed experiment profile PA'_m, said data set$\{PA'_m(k)\}$, a second error-corrected processed experiment profile PA''_m, or ~~a~~ **said** data set $\{PA''_m(k)\}$, wherein said second error-corrected processed experiment profile PA''_m comprises

said data set $\{PA''_m(k)\}$ ~~obtained by combining said first error-corrected processed experiment profile PA'_m with said processed experiment profile PA_m using a weighing factor $\{w(k)\}$, k = 1, 2, ..., N, wherein $w(k)$ is a weighing factor for the k'th measurement~~.

100. (Previously Presented) The computer program product of claim 99, wherein said processing step (a) comprises normalizing each said experiment profile XA_m and reference profile XC_m.

101. **(Currently Amended)** The computer program product of claim 100, wherein said normalizing is carried out according to the equations:

$$NA_m(k) = \frac{XA_m(k)\cdot\overline{XAC}}{\overline{XA_m}}$$

and

$$NC_m(k) = \frac{XC_m(k)\cdot\overline{XAC}}{\overline{XC_m}}$$

where $\{NA_m(k)\}$ is said first data set of said processed experiment profile PA_m, and $\{NC_m(k)\}$ is said second data set of said processed reference profile PC_m; where $\overline{XA_m}$ is an average of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents of said data set $\{XA_m(k)\}$, and $\overline{XC_m}$ is an average of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed

measurements of said plurality of different cellular constituents of data set $\{XC_m(k)\}$; and wherein $\overline{XAC}$ is an average calculated according to the equation

$$\overline{XAC} = \frac{1}{2M} \sum_{m=1}^{M} (\overline{XA_m} + \overline{XC_m}).$$

102. (Previously Presented) The computer program product of claim 101, wherein the method further comprises normalizing errors of said experiment profile XA_m and reference profile XC_m according to the equations:

$$\sigma_m^A(k) = \frac{\sigma_m^{XA}(k) \cdot \overline{XAC}}{\overline{XA_m}}$$

and

$$\sigma_m^C(k) = \frac{\sigma_m^{XC}(k) \cdot \overline{XAC}}{\overline{XC_m}}$$

where $\sigma_m^{XA}(k)$ and $\sigma_m^{XC}(k)$ are the standard errors of $XA_m(k)$ and $XC_m(k)$, respectively, and $\sigma_m^A(k)$and $\sigma_m^C(k)$ are normalized standard errors of $NA_m(k)$ and $NC_m(k)$, respectively.

103. (Previously Presented) The computer program product of claim 102, wherein the method further comprises normalizing background errors of said experiment profile XA_m and reference profile XC_m according to the equations:

$$bkgstd\,\underset{m}{A}(k) = \frac{bkg\,std\,\underset{m}{\overline{XA}}(k)\cdot\overline{XAC}}{\overline{XA_m}}$$

and

$$bkgstd\,\underset{m}{C}(k) = \frac{bkg\,std\,\underset{m}{\overline{XC}}(k)\cdot\overline{XAC}}{\overline{XC_m}}$$

where $bkgstd\,\underset{m}{XA}(k)$ and $bkgstd\,\underset{m}{XC}(k)$ are the standard background errors of $XA_m(k)$ and $XC_m(k)$, respectively, and $bkgstd\,\underset{m}{A}(k)$ and $bkgstd\,\underset{m}{C}(k)$ are normalized standard background errors of said $NA_m(k)$ and said $NC_m(k)$, respectively.

104. (**Currently Amended**) The computer program product of claim 102, wherein the method further comprises determining said averages $\overline{XA_m}$ and $\overline{XC_m}$ excluding measurements of said plurality of different cellular constituents having a value among the highest 10% of said measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents in said data sets $\{XA_m(k)\}$ and $\{XC_m(k)\}$, respectively.

105. (**Currently Amended**) The computer program product of claim 99, wherein said processing step (a) comprises:

normalizing each said experiment profile XA_m and reference profile XC_m to generate normalized data set $\{NA_m(k)\}$ and normalized data set $\{NC_m(k)\}$, respectively;

transforming said normalized data set $\{NA_m(k)\}$ to obtain a transformed data set

$\{TA_m(k)\}$, where said transformed data set $\{TA_m(k)\}$ is said first data set of said processed experiment profile PA_m; and

transforming said normalized data set $\{NC_m(k)\}$ to obtain a transformed data set $\{TC_m(k)\}$, where said transformed data set $\{TC_m(k)\}$ is said second data set of said processed reference profile PC_m;

wherein said transforming is carried out for an experiment according to equations

$$TA_m(k) = f(x) = \frac{1n\left[\frac{b^2+2\cdot a^2\cdot NA_m(k)}{a} + 2\cdot\sqrt{c^2+b^2\cdot NA_m(k)+a^2\cdot[NA_m(k)]^2}\right]}{a} + d_2$$

for $NA_m(k)>0$

and

$$TC_m(k) = f(x) = \frac{1n\left[\frac{b^2+2\cdot a^2\cdot NC_m(k)}{a} + 2\cdot\sqrt{c^2+b^2\cdot NC_m(k)+a^2\cdot[NC_m(k)]^2}\right]}{a} + d_2$$

for $NC_m(k)>0$

where d is described by equation

$$d = \frac{-1n\left[\frac{b^2}{a}+2\cdot c\right]}{a}$$

and where a is the fractional error coefficient of said experiment, b is the Poisson error coefficient of said experiment, and c is the standard deviation of background noise of said experiment.

106. **(Canceled)**

107. **(Currently Amended)** The computer program product of claim 99, wherein said processing step (a) comprises:

normalizing each said experiment profile XA_m and reference profile XC_m to generate normalized data set $\{NA_m(k)\}$ and normalized data set $\{NC_m(k)\}$, respectively;

transforming said normalized data set $\{NA_m(k)\}$ **to a new domain in which variance becomes a constant** to obtain a transformed data set $\{TA_m(k)\}$;

transforming said normalized data set $\{NC_m(k)\}$ **to a new domain in which variance becomes a constant** to obtain a transformed data set $\{TC_m(k)\}$; and

removing nonlinearity from each said transformed data sets $\{TA_m(k)\}$ and $\{TC_m(k)\}$, respectively.

108. **(Currently Amended)** The computer program product of claim 107, wherein said removing nonlinearity is carried out by a method comprising

(a1) calculating an average transformed profile of transformed experiment profiles and transformed reference profiles, wherein each of said transformed experiment profiles contains a corresponding **said** transformed data set $\{TA_m(k)\}$, and each of said transformed reference profiles contains a corresponding **said** transformed data set $\{TC_m(k)\}$; and

(a2) **calculating first differences between each of said transformed experiment profiles and said average transformed profile; calculating second differences between each of said transformed reference profiles and said**

average transformed profile; adjusting**, wherein the adjusting comprises correcting nonlinearity** each of said transformed experiment profiles based on **said** first differences between each of said transformed experiment profiles and said average transformed profile, and adjusting**, wherein the adjusting comprises correcting nonlinearity** each of said transformed reference profiles based on **said** second differences between each of said transformed reference profiles and said average transformed profile.

109. **(Currently Amended)** The computer program product of claim 108, wherein the method further comprises calculating said first differences based on the differences in a first subset of **error-model-based transformed measurements or logarithm-based** transformed measurements of said plurality of different cellular constituents between each of said transformed experiment profiles and said average transformed profile, and calculating said second differences based on the differences in a second subset of **error-model-based transformed measurements or logarithm-based** transformed measurements of said plurality of different cellular constituents between each of said transformed reference profiles and said average transformed profile.

110. **(Currently Amended)** The computer program product of claim 109, wherein each said first subset consists of **error-model-based transformed measurements or logarithm-based** transformed measurements that are ranked similarly between each of said transformed experiment profiles and said average

transformed profile, and each said second subset consists of **error-model-based transformed measurements or logarithm-based** transformed measurements that are ranked similarly between each of said transformed reference profiles and said average transformed profile.

111. **(Currently Amended)** The computer program product of claim 110, wherein said adjusting step (a2) is carried out by a method comprising:

(a2i) binning said first subset into a plurality of bins, each said bin consisting of **error-model-based transformed measurements or logarithm-based** transformed measurements of said plurality of different cellular constituents in one of said transformed experiment profiles and said average transformed profile having a value in a given range; and binning said second subset into a plurality of bins, each said bin consisting of **error-model-based transformed measurements or logarithm-based** transformed measurements of said plurality of different cellular constituents in one of said transformed reference profiles and said average transformed profile having a value in a given range;

(a2ii) calculating, in each bin of said plurality of bins, a first mean difference between a feature value of **error-model-based transformed measurements or logarithm-based** transformed measurements of said plurality of different cellular constituents in said one of said transformed experiment profiles and a feature value of said average transformed profile, and calculating a second mean difference between a feature value of **error-model-based transformed measurements or logarithm-based**

transformed measurements of said plurality of different cellular constituents in said one of said reference profiles and a feature value of the average profile;

(a2iii) determining a first curve of said first mean difference as a first function of values of **error-model-based transformed measurements or logarithm-based** transformed measurements of said plurality of different cellular constituents for said one of said transformed experiment profiles, wherein said first function is represented by, $nonlinear\_TA_m$, and determining a second curve of said second mean difference as a second function of values of **error-model-based transformed measurements or logarithm-based** transformed measurements of said plurality of different cellular constituents for said one of said transformed reference profiles, wherein said second function is represented by $nonlinear\_TC_m$; and

(a2iv) computing corrected **error-model-based transformed measurements or logarithm-based** transformed measurements of said plurality of different cellular constituents in each said transformed data set $\{TA_m(k)\}$, according to the equation:

$$TA_m^{corr}(k) = TA_m(k) - nonlinear\_TA_m(k),$$

and computing corrected **error-model-based transformed measurements or logarithm-based** transformed measurements of said plurality of different cellular constituents in each said transformed data set $\{TC_m(k)\}$, according to the equation:

$$TC_m^{corr}(k) = TC_m(k) - nonlinear\_TC_m(k),$$

where $k = 1, ..., N$; and where $\{TA_m^{corr}(k)\}$ is said first processed data set of said processed experiment profile PA_m, and $\{TC_m^{corr}(k)\}$ is said second processed data set of

said processed reference profile PC_m.

112. **(Currently Amended)** The computer program product of claim 111, wherein said processed experiment profile PA_m and said processed reference profile PC_m comprise **error-model-based transformed measurements or logarithm-based** transformed measurements of said plurality of different cellular constituents from the same experimental reaction.

113. **(Currently Amended)** The computer program product of claim 112, wherein the method further comprises calculating $\overline{PC}(k)$ according to the equation

$$\overline{PC}(k) = \frac{1}{M} \sum_{m=1}^{M} PC_m(k),$$

wherein $\{PC_m(k)\}$ comprises **error-model-based transformed measurements or logarithm-based** transformed measurements from said second processed data set $\{TC_m^{corr}(k)\}$ and calculating said differential reference profile according to the equation

$$PC_{diff}(m,k) = PC_m(k) - \overline{PC}(k)$$

and wherein said first error-corrected profile is calculated according to the equation

$$PA'_m(k) = PA_m(k) - PC_{diff}(m,k),$$

wherein $\{PA_m(k)\}$ comprises **error-model-based transformed measurements or logarithm-based** transformed measurements from said first data set $\{TA_m^{corr}(k)\}$.

114. (Previously Presented) The computer program product of claim 113, wherein the method further comprises

(d) calculating for each processed profile pair $\{PA_m, PC_m\}$, where $m \in \{1, 2, ..., M\}$, a second error-corrected experiment profile PA''_m comprising data set $\{PA''_m(k)\}$ by combining said first error-corrected experiment profile PA'_m with said processed experiment profile PA_m using a weighing factor $\{w(k)\}$, k = 1,2, ..., N, wherein w(k) is a weighing factor for the k'th measurement.

115. (Previously Presented) The computer program product of claim 114, wherein said second error-corrected experiment profile PA''_m is calculated according to the equation

$$PA''_m(k) = (1\text{-}w(k)) \cdot PA_m(k) + w(k)PA'_m(k).$$

116. (Previously Presented) The computer program product of claim 115, wherein the method further comprises determining said weighing factor according to the equation

$$w(k) = 1\text{-}e^{-0.5\left[\frac{\overline{PC(k)}}{avg\_bkgstd}\right]^2}$$

where *avg_bkgstd* is an average background standard error.

117. (Previously Presented) The computer program product of claim 116, wherein the method further comprises determining said *avg_ bkgstd* according to the

equation

$$avg\_bkgstd = \frac{1}{N}\sum_{k=1}^{N}\left[\frac{1}{M}\sum_{m=1}^{M} bkgstd(m,k)\right]$$

where *bkgstd (m, k)* is background standard error of $PC_m(k)$.

118. (Previously Presented) The computer program product of claim 113, wherein the method further comprises determining errors $\{P\sigma'_m\}$ of said first error-corrected experiment profile $\{PA'_m\}$, wherein said $\{P\sigma'_m\}$ comprises error data set $\{P\sigma'_m(k)\}$.

119. (Previously Presented) The computer program product of claim 118, wherein the method further comprises determining said error data set $\{P\sigma'_m(k)\}$ according to the equation

$$\sigma'^2_m(k) = P\sigma^2_m(k) = mixed\_P\sigma_m{}^2(k) - 2Cor(k)\cdot P\sigma_m(k)\cdot mixed\_P\sigma_m(k)$$

where $P\sigma_m(k)$ is the standard error of $A_m(k)$, and determining $mixed\_P\sigma_m(k)$ according to the equation

$$mixed\_P\sigma_m(k) = \frac{P\sigma_m(k) + (M-1)\cdot P\sigma_{ref}(k)}{M}$$

where

$$P\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_{m}^{M}(PC_m(k) - \overline{PC}(k))^2}$$

and where Cor(k) is a correlation coefficient between said processed experiment profile

PA_m and said processed reference profile PC_m.

120. (Previously Presented) The computer program product of claim 119, wherein said Cor(k) is determined according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5\left[\frac{\overline{PC(k)}}{ave\_bkgstd}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

121. (Previously Presented) The computer program product of claim 120, wherein the method further comprises determining errors $\{P\sigma"_m\}$ of said second error-corrected experiment profile $\{PA"_m\}$ wherein said $\{P\sigma"_m\}$ comprises error data set $\{P\sigma"_m(k)\}$.

122. (Previously Presented) The computer program product of claim 121, wherein the method further comprises determining said error data set $\{P\sigma"_m(k)\}$ according to the equation

$$P\sigma"_m(k) = \sqrt{[1 - w(k)] \cdot P\sigma_m^2(k) + w(k) P\sigma'^2_m(k)}$$

where $P\sigma_m(k)$ is the standard error of $PA_m(k)$, and the method further comprises determining $P\sigma'_m(k)$ according to the equation

$$P\sigma'_m(k) = \sqrt{P\sigma_m^2(k) + mixed\_P\sigma_m{}^2(k) - 2 \cdot Cor(k) \cdot P\sigma_m(k) \cdot mixed\_P\sigma_m(k)},$$

and

the method further comprises determining $mixed\_P\sigma_m(k)$ according to the equation

$$mixed\_P\sigma_m(k) = \frac{P\sigma_m(k) + (M-1)\cdot P\sigma_{ref}(k)}{M}$$

where

$$P\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_{m}^{M} (PC_m(k) - \overline{PC}(k))^2}$$

and where Cor(k) is a correlation coefficient between said processed experiment profile PA_m and said processed reference profile PC_m.

123. (Previously Presented) The computer program product of claim 122, wherein the method further comprises determining said Cor(k) according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5\left[\frac{\overline{PC}(k)}{avg\_bkgstd}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

124. (Previously Presented) The computer program product of claim 123, wherein each said pair of profiles XA_m and XC_m comprise measurements of said plurality of different cellular constituents from a two-channel microarray experiment.

125. (Previously Presented) The computer program product of claim 124, wherein said reference profiles $\{XC_m\}$, m = 1, 2, ... , M, are measured with samples

labeled with a same label.

126. (Previously Presented) The computer program product of claim 125, wherein at least one of said pairs of profiles $\{XA_m, XC_m\}$ is a virtual profile.

127. **(Currently Amended)** A computer program product for use in conjunction with a computer having a processor and a memory connected to the processor, said computer program product comprising a computer readable storage medium having a computer program mechanism encoded thereon, wherein said computer program mechanism may be loaded into the memory of said computer and cause said computer to carry out a method for generating at least one error-corrected experiment profile of at least one experiment profile A_m, where $m \in \{1, 2, ..., M\}$ in at least one of a plurality of pairs of profiles $\{A_m, C_m\}$, A_m being an experiment profile, C_m being a reference profile, where $m = 1, 2, ..., M$, M is the number of pairs of profiles, said method comprising:

~~adjusting~~ **via said differential reference profile calculated between C_m and an average reference profile $\bar{C}$ determined for profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, ..., M\}$, removing**, on a computer, **systematic cross-experiment error from** said experiment profile A_m ~~using a differential reference profile calculated between C_m and an average reference profile $\bar{C}$ determined for profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, ..., M\}$~~ to generate a first error-corrected experiment profile A'_m;

wherein said average reference profile $\vec{C}$ is an average of reference profiles $\{C_m\}$, m = 1, 2, ... , M; wherein for each m $\in$ {1, 2, ..., M}, said first error-corrected experiment profile A'_m comprises data set $\{A'_m(k)\}$, said experiment profile A_m comprises data set $\{A_m(k)\}$, said reference profile C_m comprises data set $\{C_m(k)\}$, and said average reference profile $\vec{C}$ comprises data set $\{\vec{C}(k)\}$, wherein said data set $\{A_m(k)\}$ comprises measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of a plurality of different cellular constituents measured in a sample having been subject to a first condition, said data set $\{C_m(k)\}$ comprises measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents measured in a sample having been subject to a second condition, wherein k = 1, 2, ... , N; k is an index of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of cellular constituents, N being the total number of measurements;

obtaining a data set $\{A''_m(k)\}$, wherein obtaining said data set $\{A''_m(k)\}$ comprises combining said first error-corrected experiment profile A'_m with said experiment profile A_m using a weighing factor $\{w(k)\}$, k = 1, 2, ... , N, wherein $w(k)$ is a weighing factor for a k'th measurement; and

outputting to a user, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying: said first error-corrected experiment profile A'_m, said data set $\{A'_m(k)\}$, a second error-corrected experiment profile A''_m, or ~~a~~ **said** data set $\{A''_m(k)\}$, wherein said second error-

corrected experiment profile A''_m comprises said data set $\{A''_m(k)\}$ ~~obtained by combining said first error-corrected experiment profile A'_m with said experiment profile A_m using a weighing factor $\{w(k)\}$, k = 1, 2, ... , N, wherein $w(k)$ is a weighing factor for the k'th measurement~~.

128. (Previously Presented) The computer program product of claim 88, wherein the method further comprises obtaining said transformed measurements of said data set $\{A_m(k)\}$ and said data set $\{C_m(k)\}$ for an experiment according to the equations:

$$A_m(k) = f(x) = \frac{1n\left[\frac{b^2+2\cdot a^2\cdot XA_m(k)}{a}+2\sqrt{c^2+b^2\cdot XA_m(k)+a^2\cdot[XA_m(k)]^2}\right]}{a}+d,$$

for $XA_m(k)>0$

and

$$C_m(k) = f(x) = \frac{1n\left[\frac{b^2+2\cdot a^2\cdot XC_m(k)}{a}+2\sqrt{c^2+b^2\cdot XC_m(k)+a^2\cdot[XC_m(k)]^2}\right]}{a}+d,$$

for $XC_m(k)>0$

where $\{XA_m(k)\}$ and $\{XC_m(k)\}$ are data sets comprising measurements of said plurality of different cellular constituents that when transformed produce said transformed measurements of said plurality of different cellular constituents of said data set $A_m(k)$ and said data set $C_m(k)$, respectively, where d is described by the equation:

$$d = \frac{-1n\left[\frac{b^2}{a} + 2 \cdot c\right]}{a}$$

and where a is the fractional error coefficient of said experiment, b is the Poisson error coefficient of said experiment, and c is the standard deviation of background noise of said experiment.

129. (Previously Presented) The computer program product of claim 99, wherein said processing comprises:

normalizing, transforming, and/or removing nonlinearity from measurements of said plurality of cellular constituents of said data set $\{XA_m(k)\}$ of said experiment profile XA_m, and from measurements of said plurality of cellular constituents of said data set $\{XC_m(k)\}$ of said reference profile XC_m.

130. (**Currently Amended**) A computer system comprising:

a processor; and

a memory coupled to said processor and encoding one or more programs;

wherein said one or more programs cause the processor to carry out a method for generating at least one error-corrected experiment profile of at least one experiment profile in a plurality of pairs of profiles $\{A_m,C_m\}$, where $m = 1, 2, \ldots, M$, and M is the number of the pairs of profiles; and wherein, for each $m \in \{1, 2, \ldots, M\}$, A_m is an experiment profile, and C_m is a reference profile; and wherein $\{A_m\}$ represents experiment profiles in said plurality of pairs of profiles $\{A_m,C_m\}$ and $\{C_m\}$ represents

reference profiles in said plurality of pairs of profiles $\{A_m, C_m\}$, said method comprising:

(a) calculating, on a computer, an average reference profile $\bar{C}$ of said plurality of reference profiles $\{C_m\}$ where m = 1, 2, …, M;

(b) determining, on a computer, for at least one profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, \ldots, M\}$ of said plurality of pairs of profiles $\{A_m, C_m\}$ a differential reference profile computed between C_m and $\bar{C}$;

(c) ~~adjusting~~ **via said differential reference profile determined for said profile pair, removing**, on a computer, **systematic cross-experiment error from** an experiment profile A_m of said at least one profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, \ldots, M\}$ ~~based on said differential reference profile determined for said profile pair~~ to generate a first error-corrected experiment profile A'_m for each $m \in \{1, 2, \ldots, M\}$, wherein said experiment profile A_m comprises a first data set, said reference profile C_m comprises a second data set, said average reference profile $\bar{C}$ comprises data set $\{\bar{C}(k)\}$, and said first error-corrected experiment profile A'_m comprises data set $\{A'_m(k)\}$; wherein said first data set comprises measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of a plurality of different cellular constituents measured in a sample having been subject to a first condition, said second data set comprises measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents measured in a sample having been subject to a second condition; and wherein k = 1, 2, ..., N; k is an index of measurements**, error-**

model-based transformed measurements, or **logarithm-based** transformed measurements of said plurality of different cellular constituents, N being the total number of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements;

(d) obtaining a data set {A"$_m$ (k)}, wherein obtaining said data set {A"$_m$ (k)} comprises combining said first error-corrected experiment profile A'$_m$ with said experiment profile A$_m$ using a weighing factor {*w(k)*}, k = 1, 2, ... , N, wherein *w(k)* is a weighing factor for a *k*'th measurement; and

~~(d)~~ **(e)** outputting to a user, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying: said first error-corrected experiment profile A'$_m$, said data set {A'$_m$(*k*)}, a second error-corrected experiment profile A"$_m$, or ~~a~~ **said** data set {A"$_m$ (k)}, wherein said second error-corrected experiment profile A"$_m$ comprises said data set {A"$_m$ (k)} ~~**obtained by combining said first error-corrected experiment profile A'$_m$ with said experiment profile A$_m$ using a weighing factor {*w(k)*}, k = 1, 2, ... , N, wherein *w(k)* is a weighing factor for the *k*'th measurement**~~.

131. (Previously Presented) The computer system of claim 130, wherein said steps (b) and (c) are performed for each profile pair {$A_m C_m$ } where m ϵ {1, 2, ... , M}.

132. **(Currently Amended)** The computer system of claim 131, wherein

each of said experiment profile A_m and said reference profile C_m comprises measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents from the same experimental reaction.

133. (Previously Presented) The computer system of claim 132, wherein said $\bar{C}(k)$ is calculated according to the equation

$$\bar{C}(k) = \frac{1}{M}\sum_{m=1}^{M} C_m(k)$$

wherein said differential reference profile is determined according to the equation

$$C_{diff}(m,k) = C_m(k) - \bar{C}(k)$$

and wherein said first error-corrected experiment profile A'_m is generated according to the equation

$$A'_m(k) = A_m(k) - C_{diff}(m,k)$$

wherein $\{A_m(k)\}$ is said first data set of experiment profile A_m.

134. **(Currently Amended)** The computer system of claim 133, wherein the method further comprises:

(d) calculating, for **one or more remaining profile pairs out of** ~~**each said**~~ **said** profile ~~**pair**~~ **pairs** $\{A_m, C_m\}$**,** ~~**said**~~ **a respective** second error-corrected

experiment profile A"$_m$; and

(e) outputting to, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying; said **respective** second error-corrected experiment profile A"$_m$ or said data set {A"$_m$ (k)}.

135. (Previously Presented) The computer system of claim 134, wherein said second error-corrected experiment profile A"$_m$ is calculated according to the equation

$$A''_m(k) = (1\text{-}w(k)) \cdot A_m(k) + w(k) \cdot A'_m(k).$$

136. (Previously Presented) The computer system of claim 135, wherein the method further comprises determining said weighing factor *w(k)* according to the equation

$$w(k) = 1 - e^{-0.5\left[\frac{\bar{c}(k)}{avg\_bkgstd}\right]^2}$$

where *avg_bkgstd* is an average background standard error.

137. (Previously Presented) The computer system of claim 136, wherein the method further comprises determining said *avg_bkgstd* according to the equation

$$avg\_bkgstd = \frac{1}{N}\sum_{k=1}^{N}\left[\frac{1}{M}\sum_{m=1}^{M} bkgstd(m,k)\right]$$

where *bkgstd (m, k)* is background standard error of $C_m(k)$.

138. (Previously Presented) The computer system of claim 133, wherein the method further comprises determining errors $\{\sigma'_m(k)\}$ of said data set $\{A'_m(k)\}$ in said first error-corrected experiment profile A'_m.

139. (Previously Presented) The computer system of claim 138, wherein the method further comprises determining said errors $\{\sigma'_m(k)\}$ according to the equation

$$\sigma'_m(k) = \sqrt{\sigma_m^2(k) + mixed\_\sigma_m^2(k) - 2 \cdot Cor(k) \cdot \sigma_m(k) \cdot mixed\_\sigma_m(k)}$$

where σ_m *(k)* is the standard error of $A_m(k)$, the method further comprising determining *mixed* _ σ_m *(k)* according to the equation

$$mixed\_\sigma_m(k) = \frac{\sigma_m(k) + (M-1)\cdot\sigma_{ref}(k)}{M}$$

where $\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_{m}^{M}(C_m(k) - \bar{C}(k))^2}$

and where Cor(k) is a correlation coefficient between said experiment profile A_m and said reference profile C_m.

140. (Previously Presented) The computer system of claim 139, wherein the method further comprises determining said Cor(k) according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5 \cdot \left[\frac{\bar{C}(k)}{avg\_bkgstd}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

141. (Previously Presented) The computer system of claim 136, wherein the method further comprises determining errors $\{\sigma''_m(k)\}$ of said data set $\{A''_m(k)\}$ in said second error-corrected experiment profile A''_m.

142. (Previously Presented) The computer system of claim 141, wherein said errors $\{\sigma''_m(k)\}$ are determined according to the equation

$$\sigma''_m(k) = \sqrt{[1 - w(k)] \cdot \sigma_m^2(k) + w(k)\sigma'^2_m(k)}$$

where $\sigma_m(k)$ is the standard error of $A_m(k)$, the method further comprising (i) determining $\sigma'_m(k)$ according to the equation

$$\sigma'_m(k) = \sqrt{\sigma^2_m(k) + mixed\_\sigma_m^2(k) - 2 \cdot Cor(k) \cdot \sigma_m(k) \cdot mixed\_\sigma_m(k)}, \text{ and}$$

(ii) determining $mixed\_\sigma_m(k)$ according to the equation

$$mixed\_\sigma_m(k) = \frac{\sigma_m(k) + (M-1) \cdot \sigma_{ref}(k)}{M}$$

where $\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_m^M (c_m(k) - \bar{C}(k))^2}$

and where Cor(k) is a correlation coefficient between said experiment profile A_m and

said reference profile C_m.

143. (Previously Presented) The computer system of claim 142, wherein the method further comprises determining said Cor(k) according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5 \cdot \left[\frac{\bar{c}(k)}{avg\_bkgstd}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

144. (Previously Presented) The computer system of claim 131, wherein said experiment profile A_m and said reference profile C_m of each said profile pair $\{A_m, C_m\}$ are measured in a two-channel microarray experiment.

145. (Previously Presented) The computer system of claim 144, wherein said reference profiles $\{C_m\}$, where m = 1, 2, ... , M, are measured with samples labeled with a same label.

146. (Previously Presented) The computer system of claim 131, wherein at least one of said plurality of pairs of profiles $\{A_m, C_m\}$ is a virtual profile.

147. **(Currently Amended)** The computer system of claim 130, wherein said plurality of pairs of profiles $\{A_m, C_m\}$ are transformed profiles each comprising **error-model-based transformed measurements or logarithm-based** transformed

measurements of said plurality of different cellular constituents in data set $\{A_m(k)\}$ and data set $\{C_m(k)\}$, respectively; and wherein said data set $\{A_m(k)\}$ is said first data set, and said data set $\{C_m(k)\}$ is said second data set.

148. **(Currently Amended)** The computer system of claim 130, wherein the method further comprises:

(a0) removing nonlinearity, prior to said calculating step (a), from measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents to generate said plurality of pairs of profiles $\{A_m, C_m\}$ comprising said experiment profile A_m and reference profile C_m.

149. **(Currently Amended)** The computer system of claim 148, wherein said removing step (a0) comprises:

(a0i) calculating an average profile of pre-experiment profiles $\{A_m^{pre}\}$ and pre- reference profiles $\{C_m^{pre}\}$; wherein each of said pre-experiment profiles comprises measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents measured in said sample having been subject to said first condition, which when nonlinearity is removed therefrom, produces each said experiment profile A_m; and wherein each of said pre-reference profiles comprises measurements,

error-model-based transformed measurements, or **logarithm-based** transformed measurements of said plurality of different cellular constituents measured in said sample having been subject to said second condition, which when nonlinearity is removed therefrom, produces each said reference profile C_m; and

(a0ii) **calculating first differences between each of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile; calculating second differences between each of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile;** adjusting**, wherein the adjusting comprises correcting nonlinearity,** each of said pre-experiment profiles $\{A_m^{pre}\}$ based on **said** first differences between each of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile, thereby generating each said experiment profile A_m; and adjusting**, wherein the adjusting comprises correcting nonlinearity,** each of pre-reference profiles $\{C_m^{pre}\}$ based on **said** second differences between each of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile, thereby generating each said reference profile C_m.

150. **(Currently Amended)** The computer system of claim 149, wherein the method further comprises calculating said first differences based on a first subset of said measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents in said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile; and calculating said

second differences based on a second subset of said measurements, **error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents in said pre-reference profiles $\{C_m^{pre}\}$ and said average profile.

151. **(Currently Amended)** The computer system of claim 150, wherein said first subset consists of measurements, **error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents that are ranked similarly between each of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile, and said second subset consists of measurements, **error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents that are ranked similarly between each of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile.

152. **(Currently Amended)** The computer system of claim 151, wherein said adjusting step (a0ii) is carried out by a method comprising:

(ii1) binning said first subset into a first plurality of bins, wherein each of said first plurality of bins consists of measurements, **error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents in one of said pre-experiment profiles $\{A_m^{pre}\}$ and

said average profile having a value in a given range; and binning said second subset into a second plurality of bins, wherein each of said second plurality of bins consists of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents in one of said pre-reference profiles $\{C_m^{pre}\}$and said average profile having a value in a given range;

(ii2) calculating, in each bin of said first plurality of bins, a first mean difference between a feature value of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said one of said pre-experiment profiles $\{A_m^{pre}\}$ and a feature value of said average profile, and calculating a second mean difference between a feature value of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said one of said pre-reference profiles $\{C_m^{pre}\}$ and a feature value of said average profile;

(ii3) determining a first curve of said first mean difference as a first function of values of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents for said one of said pre-experiment profiles $\{A_m^{pre}\}$,wherein said first function is represented by, $nonlinear\_A_m^{pre}$; and determining a second curve of said second mean difference as a second function of values of measurements**, error-**

model-based transformed measurements, or **logarithm-based** transformed measurements of said plurality of different cellular constituents for said one of said pre-reference profiles $\{C_m^{pre}\}$,wherein said second function is represented by $nonlinear\_C_m^{pre}$; and

(ii4) adjusting each of said pre-experiment profiles $\{A_m^{pre}\}$ according to the equation:

$$A_m(k) = A_m^{pre}(k) - nonlinear\_A_m^{pre}(k),$$

and adjusting each of said pre-reference profiles $\{C_m^{pre}\}$ according to the equation:

$$C_m(k) = C_m^{pre}(k) - nonlinear\_C_m^{pre}(k),$$

where k = 1, ... , N; and where $A_m^{pre}(k)$ and $C_m^{pre}(k)$ are data sets of each of said pre-experiment profiles $\{A_m^{pre}\}$and each of said pre-reference profiles $\{C_m^{pre}\}$, respectively; and where $A_m(k)$ and $C_m(k)$ are said first data set and said second data set, respectively.

153. **(Currently Amended)** The computer system of claim 130, wherein the method further comprises:

(a0) normalizing, prior to said calculating step (a), measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents in a pre-experiment

profile A_m^{pre} and a pre-reference profile C_m^{pre} to generate said experiment profile A_m and said reference profile C_m, respectively.

154. **(Currently Amended)** The computer system of claim 153, wherein said normalizing step (a0) comprises normalizing a data set $A_m^{pre}(k)$ and a data set $C_m^{pre}(k)$, according to the equations:

$$A_m(k) = \frac{A_m^{pre}(k) \cdot \overline{A_m^{pre}}\,\overline{C_m^{pre}}}{\overline{A_m^{pre}}}$$

and

$$C_m(k) = \frac{C_m^{pre}(k) \cdot \overline{A_m^{pre}}\,\overline{C_m^{pre}}}{\overline{C_m^{pre}}},$$

wherein said data sets $A_m^{pre}(k)$ and $C_m^{pre}(k)$ each comprises measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents, where $\overline{A_m^{pre}}$ is an average of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents in said $A_m^{pre}(k)$, and $\overline{C_m^{pre}}$ is an average of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents in said $C_m^{pre}(k)$, wherein $A_m(k)$ is said first data set, wherein $A_m(k)$ comprises normalized measurements or normalized **error-model-based transformed measurements,** or **normalized logarithm-based**

transformed measurements of said pre-experiment profile A_m^{pre}; and $C_m(k)$ is said second data set wherein $A_m(k)$ comprises normalized measurements or normalized **error-model-based transformed measurements,** or **normalized logarithm-based** transformed measurements of said reference profile C_m^{pre}; and wherein $\overline{A_m^{pre} C_m^{pre}}$ is an average calculated according to the equation

$$\overline{A_m^{pre} C_m^{pre}} = \frac{1}{2M} \sum_{m=1}^{M} (\overline{A_m^{pre}} + \overline{C_m^{pre}}).$$

155. (Previously Presented) The computer system of claim 154, wherein the method further comprises normalizing errors of said data sets $\{ A_m^{pre}(k) \}$ and $\{ C_m^{pre}(k) \}$, respectively, according to the equations:

$$\sigma_m^{NA}(k) = \frac{\sigma_m^{preA}(k) \cdot \overline{A_m^{pre} C_m^{pre}}}{\overline{A_m^{pre}}}$$

and

$$\sigma_m^{NC}(k) = \frac{\sigma_m^{preC}(k) \cdot \overline{A_m^{pre} C_m^{pre}}}{\overline{C_m^{pre}}},$$

where $\sigma_m^{preA}(k)$ and $\sigma_m^{preC}(k)$ are the standard errors of $A_m^{pre}(k)$ and $C_m^{pre}(k)$, respectively, and $\sigma_m^{NA}(k)$ and $\sigma_m^{NC}(k)$ are normalized standard errors of $A_m(k)$ and $C_m(k)$, respectively.

156. (Previously Presented) The computer system of claim 155, wherein the method further comprises normalizing background errors of said data sets $\{A_m^{pre}(k)\}$ and $\{C_m^{pre}(k)\}$, respectively, according to the equations:

$$bkgstd_m^{NA}(k) = \frac{bkgstd_m^{preA}(k) \cdot \overline{A_m^{pre}} \, \overline{C_m^{pre}}}{\overline{A_m^{pre}}}$$

and

$$bkgstd_m^{NC}(k) = \frac{bkgstd_m^{preC}(k) \cdot \overline{A_m^{pre}} \, \overline{C_m^{pre}}}{\overline{C_m^{pre}}}$$

where $bkgstd_m^{preA}(k)$ and $bkgstd_m^{preC}(k)$ are the standard background errors of $A_m^{pre}(k)$ and $C_m^{pre}(k)$, respectively, and $bkgstd_m^{NA}(k)$ and $bkgstd_m^{NC}(k)$ are normalized standard background errors of $A_m(k)$ and $C_m(k)$, respectively.

157. **(Currently Amended)** The computer system of claim 156, wherein the method further comprises calculating said averages $\overline{A_m^{pre}}$ and $\overline{C_m^{pre}}$ by excluding measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents having a value among the highest 10% of said measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents in said data sets $\{A_m^{pre}(k)\}$ and $\{C_m^{pre}(k)\}$, respectively.

158. (**Currently Amended**) A computer system comprising:

a processor; and

a memory coupled to said processor and encoding one or more programs; wherein said one or more programs cause the processor to carry out a method for generating at least one error-corrected experiment profile of at least one experiment profile in a plurality of pairs of profiles $\{XA_m, XC_m\}$, XA_m being an experiment profile, XC_m being a reference profile, where m = 1, 2, ... , M, M is the number of pairs of profiles, said method comprising:

(a) processing, on a computer, said plurality of pairs of profiles $\{XA_m, XC_m\}$ to obtain a plurality of pairs of processed profiles $\{PA_m, PC_m\}$, PA_m being a processed experiment profile, PC_m being a processed reference profile**, wherein said processing comprises normalizing at least one said experiment profile XA_m and reference profile XC_m**;

(b) calculating, on a computer, an average processed reference profile $\overline{PC}$ of processed reference profiles $\{PC_m\}$, where m = 1,2, ..., M;

(c) determining, on a computer, for at least one processed profile pair $\{PA_m, PC_m\}$ where $m \in \{1, 2, ..., M\}$ of said plurality of pairs of processed profiles $\{PA_m, PC_m\}$, where m = 1, 2, ..., M, a differential reference profile computed between PC_m and $\overline{PC}$;

(d) ~~**adjusting**~~ **via said differential reference profile determined for said at**

least one processed profile pair, removing, on a computer, **systematic cross-experiment error from** a processed experiment profile PA_m of said at least one processed profile pair $\{PA_m, PC_m\}$ where $m \in \{1, 2, ..., M\}$ ~~**using said differential reference profile determined for said at least one processed profile pair**~~ to generate a first error-corrected processed experiment profile PA'_m ; wherein for each $m \in \{1, 2, ..., M\}$, said processed experiment profile PA_m comprises a first processed data set, said processed reference profile PC_m comprises a second processed data set, said average processed reference profile $\overline{PC}$ comprises data set $\{\overline{PC}(k)\}$, said first error-corrected processed experiment profile PA'_m comprises dataset $\{PA'_m(k)\}$, said experiment profile XA_m comprises data set $\{XA_m(k)\}$, said reference profile XC_m comprises data set $\{XC_m(k)\}$, wherein said data set $\{XA_m(k)\}$ comprises measurements of a plurality of different cellular constituents measured in a sample having been subject to a first condition, said data set $\{XC_m(k)\}$ comprises measurements of said plurality of different cellular constituents measured in a sample having been subject to a second condition, and where $k = 1, 2, ..., N$; k is an index of measurements of cellular constituents, N being the total number of measurements;

(e) obtaining data set $\{PA''_m(k)\}$, wherein obtaining said data set $\{PA''_m(k)\}$, comprises combining said first error-corrected processed experiment profile PA'_m with said processed experiment profile PA_m using a weighing factor $\{w(k)\}$, $k = 1, 2, ..., N$, wherein $w(k)$ is a weighing factor for a k'th measurement; and

~~(e)~~ **(f)** outputting to a user, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying: said first error-corrected processed experiment profile PA'_m, said data set$\{ PA'_m(k)\}$, a second error-corrected processed experiment profile PA''_m, or ~~a~~ **said** data set $\{PA''_m(k)\}$, wherein said second error-corrected processed experiment profile PA''_m comprises said data set $\{PA''_m(k)\}$ ~~obtained by combining said first error-corrected processed experiment profile PA'_m with said processed experiment profile PA_m using a weighing factor $\{w(k)\}$, k = 1, 2, ..., N, wherein $w(k)$ is a weighing factor for the k'th measurement~~.

159. (Previously Presented) The computer system of claim 158, wherein said processing step (a) comprises normalizing each said experiment profile XA_m and reference profile XC_m.

160. **(Currently Amended)** The computer system of claim 159, wherein said normalizing is carried out according to the equations:

$$NA_m(k) = \frac{XA_m(k) \cdot \overline{XAC}}{\overline{XA_m}}$$

and

$$NC_m(k) = \frac{XC_m(k) \cdot \overline{XAC}}{\overline{XC_m}}$$

where $\{NA_m(k)\}$ is said first data set of said processed experiment profile PA_m, and

$\{NC_m(k)\}$ is said second data set of said processed reference profile PC_m; where $\overline{XA_m}$ is an average of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents of said data set $\{XA_m(k)\}$, and $\overline{XC_m}$ is an average of measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents of data set $\{XC_m(k)\}$; and wherein $\overline{XAC}$ is an average calculated according to the equation

$$\overline{XAC} = \frac{1}{2M} \sum_{m=1}^{M} (\overline{XA_m} + \overline{XC_m}).$$

161. (Previously Presented) The computer system of claim 160, wherein the method further comprises normalizing errors of said experiment profile XA_m and reference profile XC_m according to the equations:

$$\sigma_m^A(k) = \frac{\sigma_m^{XA}(k) \cdot \overline{XAC}}{\overline{XA_m}}$$

and

$$\sigma_m^C(k) = \frac{\sigma_m^{XC}(k) \cdot \overline{XAC}}{\overline{XC_m}}$$

where $\sigma_m^{XA}(k)$ and $\sigma_m^{XC}(k)$ are the standard errors of $XA_m(k)$ and $XC_m(k)$, respectively, and $\sigma_m^A(k)$and $\sigma_m^C(k)$ are normalized standard errors of $NA_m(k)$ and $NC_m(k)$, respectively.

162. (Previously Presented) The computer system of claim 161, wherein the method further comprises normalizing background errors of said experiment profile XA_m and reference profile XC_m according to the equations:

$$bkgstd\,\frac{A}{m}(k) = \frac{bkgstd\,\frac{XA}{m}(k)\cdot\overline{XAC}}{\overline{XA_m}}$$

and

$$bkgstd\,\frac{C}{m}(k) = \frac{bkgstd\,\frac{XC}{m}(k)\cdot\overline{XAC}}{\overline{XC_m}}$$

where $bkgstd\,\frac{XA}{m}(k)$ and $bkgstd\,\frac{XC}{m}(k)$ are the standard background errors of $XA_m(k)$ and $XC_m(k)$, respectively, and $bkgstd\,\frac{A}{m}(k)$ and $bkgstd\,\frac{C}{m}(k)$ are normalized standard background errors of said $NA_m(k)$ and said $NC_m(k)$, respectively.

163. **(Currently Amended)** The computer system of claim 161, wherein the method further comprises determining said averages $\overline{XA_m}$ and $\overline{XC_m}$ excluding measurements of said plurality of different cellular constituents having a value among the highest 10% of said measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents in said data sets $\{XA_m(k)\}$ and $\{XC_m(k)\}$, respectively.

164. (**Currently Amended**) The computer system of claim 158, wherein said processing step (a) comprises:

normalizing each said experiment profile XA_m and reference profile XC_m to generate normalized data set $\{NA_m(k)\}$ and normalized data set $\{NC_m(k)\}$, respectively;

transforming said normalized data set $\{NA_m(k)\}$ to obtain a transformed data set $\{TA_m(k)\}$, where said transformed data set $\{TA_m(k)\}$ is said first data set of said processed experiment profile PA_m; and

transforming said normalized data set $\{NC_m(k)\}$ to obtain a transformed data set $\{TC_m(k)\}$, where said transformed data set $\{TC_m(k)\}$ is said second data set of said processed reference profile PC_m;

wherein said transforming is carried out for an experiment according to equations

$$TA_m(k) = f(x) = \frac{1n\left[\frac{b^2+2\cdot a^2\cdot NA_m(k)}{a} + 2\cdot\sqrt{c^2+b^2\cdot NA_m(k)+a^2\cdot[NA_m(k)]^2}\right]}{a} + d_2$$

for $NA_m(k)>0$

and

$$TC_m(k) = f(x) = \frac{1n\left[\frac{b^2+2\cdot a^2\cdot NC_m(k)}{a} + 2\cdot\sqrt{c^2+b^2\cdot NC_m(k)+a^2\cdot[NC_m(k)]^2}\right]}{a} + d_2$$

for $NC_m(k)>0$

where d is described by equation

$$d = \frac{-1n\left[\frac{b^2}{a}+2\cdot c\right]}{a}$$

and where a is the fractional error coefficient of said experiment, b is the

Poisson error coefficient of said experiment, and *c* is the standard deviation of background noise of said experiment.

165. **(Canceled)**

166. **(Currently Amended)** The computer system of claim 158, wherein said processing step (a) comprises:

normalizing each said experiment profile XA_m and reference profile XC_m to generate normalized data set $\{NA_m(k)\}$ and normalized data set $\{NC_m(k)\}$, respectively;

transforming said normalized data set $\{NA_m(k)\}$ to obtain a transformed data set $\{TA_m(k)\}$;

transforming said normalized data set $\{NC_m(k)\}$ to obtain a transformed data set $\{TC_m(k)\}$; and

removing nonlinearity from each said transformed data sets $\{TA_m(k)\}$ and $\{TC_m(k)\}$, respectively;

wherein said transforming is carried out for an experiment according to equations

$$TA_m(k) = f(x) = \frac{1n\left[\frac{b^2+2\cdot a^2\cdot NA_m(k)}{a} + 2\cdot\sqrt{c^2+b^2\cdot NA_m(k)+a^2\cdot[NA_m(k)]^2}\right]}{a} + d_2$$

for $NA_m(k)>0$

and

$$TC_m(k) = f(x) = \frac{1n\left[\frac{b^2+2\cdot a^2\cdot NC_m(k)}{a} + 2\cdot\sqrt{c^2+b^2\cdot NC_{m2}(k)+a^2\cdot[NC_m(k)]^2}\right]}{a} + d_2$$

for $NC_m(k)>0$

where d is described by equation

$$d = \frac{-1n\left[\frac{b^2}{a}+2\cdot c\right]}{a}$$

and where a is the fractional error coefficient of said experiment, b is the Poisson error coefficient of said experiment, and c is the standard deviation of background noise of said experiment.

167. **(Currently Amended)** The computer system of claim 166, wherein said removing nonlinearity is carried out by a method comprising

(a1) calculating an average transformed profile of transformed experiment profiles and transformed reference profiles, wherein each of said transformed experiment profiles contains a corresponding **error-model-based transformed or logarithm-based** transformed data set $\{TA_m(k)\}$, and each of said transformed reference profiles contains a corresponding **error-model-based transformed measurements or logarithm-based** transformed data set $\{TC_m(k)\}$; and

(a2) **calculating first differences between each of said transformed experiment profiles and said average transformed profile; calculating second differences between each of said transformed reference profiles and said average transformed profile;** adjusting**, wherein the adjusting comprises**

correcting nonlinearity each of said transformed experiment profiles based on **said** first differences between each of said transformed experiment profiles and said average transformed profile, and adjusting**, wherein the adjusting comprises correcting nonlinearity** each of said transformed reference profiles based on **said** second differences between each of said transformed reference profiles and said average transformed profile.

168. **(Currently Amended)** The computer system of claim 167, wherein the method further comprises calculating said first differences based on the differences in a first subset of **error-model-based transformed measurements, or logarithm-based** transformed measurements of said plurality of different cellular constituents between each of said transformed experiment profiles and said average transformed profile, and calculating said second differences based on the differences in a second subset of **error-model-based transformed measurements, or logarithm-based** transformed measurements of said plurality of different cellular constituents between each of said transformed reference profiles and said average transformed profile.

169. (Previously Presented) The computer system of claim 168, wherein each said first subset consists of transformed measurements that are ranked similarly between each of said transformed experiment profiles and said average transformed profile, and each said second subset consists of transformed measurements that are ranked similarly between each of said transformed reference profiles and said average transformed profile.

170. **(Currently Amended)** The computer system of claim 169, wherein said adjusting step (a2) is carried out by a method comprising:

(a2i) binning said first subset into a plurality of bins, each said bin consisting of **error-model-based transformed measurements or logarithm-based** transformed measurements of said plurality of different cellular constituents in one of said transformed experiment profiles and said average transformed profile having a value in a given range; and binning said second subset into a plurality of bins, each said bin consisting of **error-model-based transformed measurements or logarithm-based** transformed measurements of said plurality of different cellular constituents in one of said transformed reference profiles and said average transformed profile having a value in a given range;

(a2ii) calculating, in each bin of said plurality of bins, a first mean difference between a feature value of **error-model-based transformed measurements or logarithm-based** transformed measurements of said plurality of different cellular constituents in said one of said transformed experiment profiles and a feature value of said average transformed profile, and calculating a second mean difference between a feature value of **error-model-based transformed measurements or logarithm-based** transformed measurements of said plurality of different cellular constituents in said one of said reference profiles and a feature value of the average profile;

(a2iii) determining a first curve of said first mean difference as a first function of values of **error-model-based transformed measurements or logarithm-based** transformed measurements of said plurality of different cellular constituents for said one

of said transformed experiment profiles, wherein said first function is represented by, *nonlinear_TA$_m$,* and determining a second curve of said second mean difference as a second function of values of **error-model-based transformed measurements or logarithm-based** transformed measurements of said plurality of different cellular constituents for said one of said transformed reference profiles, wherein said second function is represented by *nonlinear_TC$_m$;* and

(a2iv) computing corrected **error-model-based transformed measurements or logarithm-based** transformed measurements of said plurality of different cellular constituents in each said transformed data set {TA$_m$(k)}, according to the equation:

$$TA_m^{corr}(k) = TA_m(k) - nonlinear\_TA_m(k),$$

and computing corrected **error-model-based transformed measurements or logarithm-based** transformed measurements of said plurality of different cellular constituents in each said transformed data set {TC$_m$(k)}, according to the equation:

$$TC_m^{corr}(k) = TC_m(k) - nonlinear\_TC_m(k),$$

where k = 1, ..., N; and where $\{TA_m^{corr}(k)\}$ is said first processed data set of said processed experiment profile PA$_m$, and $\{TC_m^{corr}(k)\}$ is said second processed data set of said processed reference profile PC$_m$.

171. (**Currently Amended**) The computer system of claim 170, wherein said processed experiment profile PA$_m$ and said processed reference profile PC$_m$ comprise **error-model-based transformed measurements or logarithm-based** transformed

measurements of said plurality of different cellular constituents from the same experimental reaction.

172. **(Currently Amended)** The computer system of claim 171, wherein the method further comprises calculating $\overline{PC}(k)$ according to the equation

$$\overline{PC}(k) = \frac{1}{M} \sum_{m=1}^{M} PC_m(k),$$

wherein $\{PC_m(k)\}$ comprises **error-model-based transformed measurements or logarithm-based** transformed measurements from said second processed data set $\{TC_m^{corr}(k)\}$ and calculating said differential reference profile according to the equation

$$PC_{diff}(m,k) = PC_m(k) - \overline{PC}(k)$$

and wherein said first error-corrected profile is calculated according to the equation

$$PA'_m(k) = PA_m(k) - PC_{diff}(m,k),$$

wherein $\{PA_m(k)\}$ comprises **error-model-based transformed measurements or logarithm-based** transformed measurements from said first data set $\{TA_m^{corr}(k)\}$.

173. (Previously Presented) The computer system of claim 172, wherein the method further comprises

(d) calculating for each processed profile pair $\{PA_m, PC_m\}$, where $m \in \{1, 2, ..., M\}$, a second error-corrected experiment profile PA''_m comprising data set $\{PA''_m(k)\}$ by

combining said first error-corrected experiment profile PA'_m with said processed experiment profile PA_m using a weighing factor $\{w(k)\}$, k = 1,2, ..., N, wherein $w(k)$ is a weighing factor for the k'th measurement.

174. (Previously Presented) The computer system of claim 173, wherein said second error-corrected experiment profile PA''_m is calculated according to the equation

$$PA''_m(k) = (1\text{-}w(k)) \cdot PA_m(k) + w(k)PA'_m(k).$$

175. (Previously Presented) The computer system of claim 174, wherein the method further comprises determining said weighing factor according to the equation

$$w(k) = 1\text{-}e^{-0.5\left[\frac{\overline{PC}(k)}{avg\_bkgstd}\right]^2}$$

where *avg_bkgstd* is an average background standard error.

176. (Previously Presented) The computer system of claim 175, wherein the method further comprises determining said *avg_ bkgstd* according to the equation

$$avg\_bkgstd = \frac{1}{N}\sum_{k=1}^{N}\left[\frac{1}{M}\sum_{m=1}^{M} bkgstd(m,k)\right]$$

where *bkgstd (m, k)* is background standard error of $PC_m(k)$.

177. (Previously Presented) The computer system of claim 172, wherein the method further comprises determining errors $\{P\sigma'_m\}$ of said first error-corrected experiment profile $\{PA'_m\}$, wherein said $\{P\sigma'_m\}$ comprises error data set $\{P\sigma'_m(k)\}$.

178. (Previously Presented) The computer system of claim 177, wherein the method further comprises determining said error data set $\{P\sigma'_m(k)\}$ according to the equation

$$\sigma'_m(k) = \sqrt{P\sigma_m^2(k) = mixed\_P\sigma_m{}^2(k) - 2Cor(k) \cdot P\sigma_m(k) \cdot mixed\_P\sigma_m(k)}$$

where $P\sigma_m(k)$ is the standard error of $A_m(k)$, and determining $mixed\_P\sigma_m(k)$ according to the equation

$$mixed\_P\sigma_m(k) = \frac{P\sigma_m(k) + (M-1)\cdot P\sigma_{ref}(k)}{M}$$

where

$$P\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_{m}^{M} (PC_m(k) - \overline{PC}(k))^2}$$

and where Cor(k) is a correlation coefficient between said processed experiment profile PA_m and said processed reference profile PC_m.

179. (Previously Presented) The computer system of claim 178, wherein said Cor(k) is determined according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5\left[\frac{\overline{PC}(k)}{avg\_bkgstd}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

180. (Previously Presented) The computer system of claim 179, wherein the

method further comprises determining errors $\{P\sigma"_m\}$ of said second error-corrected experiment profile $\{PA"_m\}$ wherein said $\{P\sigma"_m\}$ comprises error data set $\{P\sigma"_m(k)\}$.

181. (Previously Presented) The computer system of claim 180, wherein the method further comprises determining said error data set $\{P\sigma"_m(k)\}$ according to the equation

$$P\sigma"_m(k) = \sqrt{[1 - w(k)] \cdot P\sigma_m^2(k) + w(k)P\sigma'^2_m(k)}$$

where $P\sigma_m(k)$ is the standard error of $PA_m(k)$, and the method further comprises determining $P\sigma'_m(k)$ according to the equation

$$P\sigma'_m(k) = \sqrt{P\sigma_m^2(k) + mixed\_P\sigma_m{}^2(k) - 2 \cdot Cor(k) \cdot P\sigma_m(k) \cdot mixed\_P\sigma_m(k)},$$

and

the method further comprises determining $mixed\_P\sigma_m(k)$ according to the equation

$$mixed\_P\sigma_m(k) = \frac{P\sigma_m(k) + (M-1) \cdot P\sigma_{ref}(k)}{M}$$

where

$$P\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_{m}^{M} (PC_m(k) - \overline{PC}(k))^2}$$

and where Cor(k) is a correlation coefficient between said processed experiment profile PA_m and said processed reference profile PC_m.

182. (Previously Presented) The computer system of claim 181, wherein the method further comprises determining said Cor(k) according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5\left[\frac{\overline{PC}(k)}{avg\_bkgstd}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

183. (Previously Presented) The computer system of claim 182, wherein each said pair of profiles XA_m and XC_m comprise measurements of said plurality of different cellular constituents from a two-channel microarray experiment.

184. (Previously Presented) The computer system of claim 183, wherein said reference profiles $\{XC_m\}$, m = 1, 2, ... , M, are measured with samples labeled with a same label.

185. (Previously Presented) The computer system of claim 184, wherein at least one of said pairs of profiles $\{XA_m, XC_m\}$ is a virtual profile.

186. **(Currently Amended)** A computer system comprising:

a processor; and

a memory coupled to said processor and encoding one or more programs;

wherein said one or more programs cause the processor to carry out a method for generating at least one error-corrected experiment profile of at least one

experiment profile A_m, where $m \in \{1, 2, ..., M\}$ in at least one of a plurality of pairs of profiles $\{A_m, C_m\}$, A_m being an experiment profile, C_m being a reference profile, where $m = 1, 2, ..., M$, M is the number of pairs of profiles, said method comprising:

~~adjusting~~ **via said differential reference profile calculated between C_m and an average reference profile $\bar{C}$ determined for profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, ..., M\}$, removing**, on a computer, **systematic cross-experiment error from** said experiment profile A_m ~~using a differential reference profile calculated between C_m and an average reference profile $\bar{C}$ determined for profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, ..., M\}$~~ to generate a first error-corrected experiment profile A'_m; wherein said average reference profile $\bar{C}$ is an average of reference profiles $\{C_m\}$, $m = 1, 2, ..., M$; wherein for each $m \in \{1, 2, ..., M\}$, said first error-corrected experiment profile A'_m comprises data set $\{A'_m(k)\}$, said experiment profile A_m comprises data set $\{A_m(k)\}$, said reference profile C_m comprises data set $\{C_m(k)\}$, and said average reference profile $\bar{C}$ comprises data set $\{\bar{C}(k)\}$, wherein said data set $\{A_m(k)\}$ comprises measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of a plurality of different cellular constituents measured in a sample having been subject to a first condition, said data set $\{C_m(k)\}$ comprises measurements**, error-model-based transformed measurements,** or **logarithm-based** transformed measurements of said plurality of different cellular constituents measured in a sample having been subject to a second

condition, wherein k = 1, 2, ... , N; k is an index of measurements, **error-model-based transformed measurements,** or **logarithm-based** transformed measurements of cellular constituents, N being the total number of measurements;

obtaining data set $\{A''_m(k)\}$, wherein obtaining said data set $\{A''_m(k)\}$ comprises combining said first error-corrected experiment profile A'_m with said experiment profile A_m using a weighing factor $\{w(k)\}$, k = 1, 2, ... , N, wherein $w(k)$ is a weighing factor for a k'th measurement; and

outputting to a user, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying: said first error-corrected experiment profile A'_m, said data set $\{A'_m(k)\}$, a second error-corrected experiment profile A''_m, or ~~a~~ **said** data set $\{A''_m(k)\}$, wherein said second error-corrected experiment profile A''_m comprises said data set $\{A''_m(k)\}$ ~~**obtained by combining said first error-corrected experiment profile A'_m with said experiment profile A_m using a weighing factor $\{w(k)\}$, k = 1, 2, ... , N, wherein $w(k)$ is a weighing factor for the k'th measurement**~~.

187. **(Currently Amended)** The computer system of claim 147, wherein the method further comprises obtaining said **error-model-based** transformed measurements of said data set $\{A_m(k)\}$ and said data set $\{C_m(k)\}$ for an experiment according to the equations:

$$A_m(k) = f(x) = \frac{1\pi\left[\frac{b^2 + z\cdot a^2 \cdot XA_m(k)}{a} + 2\cdot\sqrt{c^2 + b^2 \cdot XA_m(k) + a^2\cdot[XA_m(k)]^2}\right]}{a} + d,$$

for $XA_m(k)>0$

and

$$C_m(k) = f(x) = \frac{1n\left[\frac{b^2+z\cdot a^2\cdot XC_m(k)}{a}+2\sqrt{c^2+b^2\cdot XC_m(k)+a^2\cdot[XC_m(k)]^2}\right]}{\alpha}+d,$$

for $XC_m(k)>0$

where $\{XA_m(k)\}$ and $\{XC_m(k)\}$ are data sets comprising measurements of said plurality of different cellular constituents that when transformed produce said **error-model-based** transformed measurements of said plurality of different cellular constituents of said data set $A_m(k)$ and said data set $C_m(k)$, respectively, where d is described by the equation:

$$d = \frac{-1n\left[\frac{b^2}{a}+2\cdot c\right]}{\alpha}$$

and where a is the fractional error coefficient of said experiment, b is the Poisson error coefficient of said experiment, and c is the standard deviation of background noise of said experiment.

188. (Previously Presented) The computer system of claim 158, wherein said processing comprises:

normalizing, transforming, and/or removing nonlinearity from measurements of said plurality of cellular constituents of said data set $\{XA_m(k)\}$ of said experiment profile XA_m, and from measurements of said plurality of cellular constituents of said data set $\{XC_m(k)\}$ of said reference profile XC_m.